

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 6, 2002, 10:04:11 ; Search time 33 Seconds

(Without alignments)
429.846 Million cell updates/sec

Title: US-09-835-922-2

Perfect score: 1778
Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SODNRKEDGDPNEETPM 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1778	100.0	342	1 P2YC_HUMAN	Q9H244 homo sapien
2	1748	98.3	342	1 P2YC_MACEA	Q95K63 macaca fasc
3	1555.5	87.5	347	1 P2YC_MOUSE	Q9CPY9 mus musculu
4	1528.5	86.0	343	1 P2YC_RAT	Q9EPY4 ratu musculu
5	772	43.4	338	1 P2YX_HUMAN	Q15391 homo sapien
6	741.5	41.7	338	1 P2YX_MOUSE	Q9SE96 mus musculu
7	694	39.0	305	1 P2YX_RAT	Q35881 ratu musculu
8	488	27.4	319	1 H963_HUMAN	Q14626 homo sapien
9	411.5	23.1	375	1 GP34_MOUSE	Q9R1K6 mus musculu
10	409.5	23.0	361	1 GP34_HUMAN	Q9UP65 homo sapien
11	394	22.2	342	1 PAFR_HUMAN	P25105 homo sapien
12	392.5	22.1	342	1 PAFR_CAVPO	P21556 cavia porce
13	379.5	21.3	361	1 EB12_HUMAN	P32249 homo sapien
14	367	20.6	345	1 CLT2_PIG	Q95N03 sus scrofa
15	366	20.6	341	1 PAFR_MOUSE	Q62035 mus musculu
16	362	20.4	341	1 PAFR_RAT	P46002 ratu musculu
17	357.5	19.5	308	1 P2Y5_CHICK	P32250 gallu musculu
18	347.5	19.5	346	1 CLT2_HUMAN	Q9H875 homo sapien
19	347.5	19.5	537	1 P2Y8_XENLA	P79928 xenopus lae
20	344	19.3	309	1 CLT2_MOUSE	Q92081 mus musculu
21	339.5	19.1	309	1 CLT2_RAT	Q92493 ratu musculu
22	339	19.1	359	1 AG2R_BOVIN	P25104 bos taurus
23	338	19.0	344	1 P2Y5_HUMAN	P33657 homo sapien
24	334	18.8	359	1 AG2R_SHEEP	Q77590 ovis aries
25	334	18.8	367	1 GP17_HUMAN	Q13304 homo sapien
26	329	18.5	359	1 AG2S_HUMAN	Q13725 homo sapien
27	328	18.4	340	1 CLT1_PIG	Q95N02 sus scrofa
28	327	18.4	359	1 AG2R_PIG	P30555 sus scrofa
29	326	18.3	359	1 AG2R_CANFA	P43240 canis famli
30	325.5	18.3	359	1 PAR2_MOUSE	P55086 mus musculu
31	325	18.3	359	1 AG2R_RABIT	P49766 cryocolagus
32	321	18.1	359	1 AG2R_HUMAN	P30556 homo sapien
33	320	18.0	359	1 AG2R_CAVPO	Q9W266 cavia porce

34	320	18.0	370	1 P2Y9_HUMAN	Q96577 homo sapien
35	319.5	18.0	365	1 GP68_HUMAN	Q15743 homo sapien
36	319	17.9	359	1 AG28_RAT	P25095 ratu musculu
37	319	17.9	359	1 AG28_MOUSE	P29089 ratu musculu
38	318	17.9	359	1 AG28_MOUSE	P29754 mus musculu
39	318	17.9	361	1 P2Y4_MOUSE	Q91167 mus musculu
40	316.5	17.8	398	1 OPRM_RAT	P33535 ratu musculu
41	316	17.8	359	1 AG2S_MOUSE	P29755 mus musculu
42	316	17.8	377	1 APJ_RAT	Q91H93 ratu musculu
43	316	17.8	397	1 PAR2_RAT	Q63645 ratu musculu
44	313.5	17.6	380	1 APJ_HUMAN	P35414 homo sapien
45	313.5	17.6	401	1 OPRM_PIG	Q95247 sus scrofa

ALIGNMENTS

RESULT 1
ID P2YC_HUMAN STANDARD: PRT; 342 AA.
AC Q9H244;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE P2Y purinocceptor 12 (P2Y12) (P2Y12 platelet ADP receptor) (P2Y(ADP))
DE (ADP-glucose receptor) (ADPG-R) (P2Y(AC)) (P2Y(AC))
DE (SP1999).
GN P2RY12 OR HORK3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21037966; PubMed-11196645;
RA Hollopeter G., Jantzen H.-M., Vincent D., Li G., England L.,
RA Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan D.J.,
RA Conley P.B.;
RT "Identification of the platelet ADP receptor targeted by
RT antithrombotic drugs";
RL Nature 409:202-207(2001).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE-Hypothalamus;
RX MEDLINE-21269433; PubMed-11104774;
RA Zhang F.L., Luo L., Gustafson E., Lachowicz J., Smith M., Qiao X.,
RA Liu Y.-H., Chen G., Pramanik B., Laz T.M., Palmer K., Bayne M.,
RA Monsma F.J. Jr.;
RT "ADP is the cognate ligand for the orphan G protein-coupled receptor
RT SP1999";
RL J. Biol. Chem. 276:8608-8615(2001).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE-21394281; PubMed-11502873;
RA Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.-I.,
RA Ohishi T., Soga T., Matsushima H., Furutachi K.;
RT "Molecular cloning of the platelet P2Y(AC) ADP receptor:
RT pharmacological comparison with another ADP receptor, the P2Y1
RT receptor";
RL Mol. Pharmacol. 60:432-439(2001).
[4]
RP SEQUENCE FROM N.A.
RA Reinisch H.R., Nothacker H.-P., Wang Z., Zeng J., Ehler F.J.,
RA Clivelli O.;
RT "ADP-glucose activates a G-protein coupled receptor and inhibits
RT smooth muscle contractions";
RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takaue H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence";

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A..
 RC
 RC TISSUE-Prostate:
 RA Strauberg R.:
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
 CC inhibit the adenyllyl cyclase second messenger system. Not
 CC activated by UDP and UTP. Involved in platelets aggregation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Highly expressed in the platelets, lower
 CC levels in the brain, lowest levels in the lung, appendix,
 CC pituitary and adrenal gland. Expressed in the spinal cord and in
 CC the fetal brain.
 CC
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).

DR	EMBL	AF313449	AAC48944.1	-	-	-
DR	EMBL	AF321815	AAK00948.1	-	-	-
DR	EMBL	AB052684	BAB60824.1	-	-	-
DR	EMBL	AF310685	AAL32292.1	-	-	-
DR	EMBL	AB083586	BAB89309.1	-	-	-
DR	EMBL	BC017898	AAH17898.1	-	-	-
DR	MIM	600515	-	-	-	-
DR	InterPro	IPR002076	GPCR_Rhodpsn	-	-	-
DR	Pfam	PF00001	7tm_1	1	1	1
DR	PRINTS	PR00237	GPCRHODOPSIN	-	-	-
DR	PROSITE	PS00237	G_PROTEIN_RECPT_F1_1	FALSE	NEG.	-
DR	PROSITE	PS50262	G_PROTEIN_RECPT_F1_2	1	-	-
KW	G-protein coupled receptor	transmembrane protein	glycoprotein	-	-	-
FT	DOMAIN	1	25	-	-	-
FT	TRANSMEM	26	46	-	-	-
FT	DOMAIN	47	58	-	-	-
FT	TRANSMEM	59	79	-	-	-
FT	DOMAIN	80	99	-	-	-
FT	TRANSMEM	100	120	-	-	-
FT	DOMAIN	121	142	-	-	-
FT	TRANSMEM	143	163	-	-	-
FT	DOMAIN	164	191	-	-	-
FT	TRANSMEM	192	212	-	-	-
FT	DOMAIN	213	233	-	-	-
FT	TRANSMEM	234	254	-	-	-
FT	DOMAIN	255	281	-	-	-
FT	TRANSMEM	282	302	-	-	-
FT	DOMAIN	303	342	-	-	-
FT	DISULFID	97	175	-	-	-
FT	CARBOHYD	6	6	-	-	-
FT	CARBOHYD	13	13	-	-	-
QO	SEQUENCE	342 AA	39438 MW	855302746C89176D CRC64	-	-

Query Match	100.0%;	Score 1778;	DB 1;	Length 342;
Best Local Similarity	100.0%;	Pred. No. 1.5e-112;		
Matches 342;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	QMAVDNLTSAGNSLCTRDYKINQVLEPPLLYTLVFWGVIITNGLARIFEQIRSKSNFI	60
Db	1	QMAVDNLTSAGNSLCTRDYKINQVLEPPLLYTLVFWGVIITNGLARIFEQIRSKSNFI	60
Qy	121	DRYQKTRRPFKTSNPKNLGAKILISVIYAMFPLLSLPMNIIITNRQDRDNVVKCSPLKS	180
Db	121	DRYQKTRRPFKTSNPKNLGAKILISVIYAMFPLLSLPMNIIITNRQDRDNVVKCSPLKS	180

QY	181	EFGLVMEHINWYIQVLEFWINELLVYCYTLIRKELRYSVRRRGVKKPKRVNKKVFL	240
	181	EFGLVMEHINWYIQVLEFWINELLVYCYTLIRKELRYSVRRRGVKKPKRVNKKVFL	240
Db	181	EFGLVMEHINWYIQVLEFWINELLVYCYTLIRKELRYSVRRRGVKKPKRVNKKVFL	240
QY	241	IIAVEFCFVPFHARIPYTLISQTRDVFCDCTAENTLPEYKESTLMTLSLACDLPITYEF	300
	241	IIAVEFCFVPFHARIPYTLISQTRDVFCDCTAENTLPEYKESTLMTLSLACDLPITYEF	300
Db	241	IIAVEFCFVPFHARIPYTLISQTRDVFCDCTAENTLPEYKESTLMTLSLACDLPITYEF	300
QY	301	LCKSFRRSLISMLCKPNSATSLSDONRKKRKDDGDPNHEETPM	342
	301	LCKSFRRSLISMLCKPNSATSLSDONRKKRKDDGDPNHEETPM	342
Db	301	LCKSFRRSLISMLCKPNSATSLSDONRKKRKDDGDPNHEETPM	342

RESULT

ID	P2YC_MACEA	STANDARD;	PRT;	342 AA
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DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

P2RY12.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei

Cercopithecinae; *Macaca*.

```

Oa  MODL_JAARD-2041
RN  [1]

```

RC TISSUE=Frontal cortex, and Medulla oblongata;
RP SEQUENCE FROM N.A.

RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;

RT Isolates: "1" libraries: "1"

Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

cc inhibit the adenylyl cyclase second messenger system (By
cc similarity)

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS

CC

CC

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.....

DR EMBL; AB062981; BAB60747.1; -.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR01569; P2Y12PRNCPTR.
DR PRINTS; PR00237; GFCRKHDOFSN.
DR PRINTS; PR01569; P2Y12PRNCPTR.

```
DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; FALSE_NEG
DR PRINIS; PRO1055; ODFGLCCOSER.
```

DR PROSITE; PS50262; G_PROTEIN_RECEPT_1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein

ET	25	EXTRACELLULAR (POTENTIAL
ET	1	DOMAIN
TRANSMEM	46	1 (POTENTIAL)
ET	26	

FT	47	58	CYTOPLASMIC (POTENTIAL).
FT	59	79	2 (POTENTIAL)
DOMAIN			
TRANSMEM			

ET	80	99	EXTRACELLULAR (POTENTIAL
DOMAIN	100	120	3 (POTENTIAL)
TRANSMEM			

FT	DOMAIN	121	142	CYTOPLASMIC (POTENTIAL).
EM	EMBO/NOV	143	163	4 (CYTOPLASMIC)

FT	DOMAIN	164	191	EXTRACELLULAR (POTENTIAL

	FT	DOMAIN	CYTOPLASMIC (POTENTIAL).
2	202	213	233

FT	DOMAIN	255	281	EXTRACELLULAR (POTENTIAL
21	ANTHELMINTIC	204	204	0 (POLYMERIC).

Run	Time (min)	Flow Rate (ml/min)	Temperature (°C)	Pressure (atm)	Detector Response
1	10	1.0	30	1.2	0.5
2	20	1.0	30	1.2	1.2
3	30	1.0	30	1.2	2.1
4	40	1.0	30	1.2	3.5
5	50	1.0	30	1.2	5.2
6	60	1.0	30	1.2	7.8
7	70	1.0	30	1.2	10.5
8	80	1.0	30	1.2	13.2
9	90	1.0	30	1.2	15.8
10	100	1.0	30	1.2	18.5
11	110	1.0	30	1.2	21.2
12	120	1.0	30	1.2	24.0
13	130	1.0	30	1.2	26.8
14	140	1.0	30	1.2	29.5
15	150	1.0	30	1.2	32.2
16	160	1.0	30	1.2	35.0
17	170	1.0	30	1.2	37.8
18	180	1.0	30	1.2	40.5
19	190	1.0	30	1.2	43.2
20	200	1.0	30	1.2	46.0
21	210	1.0	30	1.2	48.8
22	220	1.0	30	1.2	51.5
23	230	1.0	30	1.2	54.2
24	240	1.0	30	1.2	57.0
25	250	1.0	30	1.2	59.8
26	260	1.0	30	1.2	62.5
27	270	1.0	30	1.2	65.2
28	280	1.0	30	1.2	68.0
29	290	1.0	30	1.2	70.8
30	300	1.0	30	1.2	73.5
31	310	1.0	30	1.2	76.2
32	320	1.0	30	1.2	79.0
33	330	1.0	30	1.2	81.8
34	340	1.0	30	1.2	84.5
35	350	1.0	30	1.2	87.2
36	360	1.0	30	1.2	90.0
37	370	1.0	30	1.2	92.8
38	380	1.0	30	1.2	95.5
39	390	1.0	30	1.2	98.2
40	400	1.0	30	1.2	101.0
41	410	1.0	30	1.2	103.8
42	420	1.0	30	1.2	106.5
43	430	1.0	30	1.2	109.2
44	440	1.0	30	1.2	112.0
45	450	1.0	30	1.2	114.8
46	460	1.0	30	1.2	117.5
47	470	1.0	30	1.2	120.2
48	480	1.0	30	1.2	123.0
49	490	1.0	30	1.2	125.8
50	500	1.0	30	1.2	128.5
51	510	1.0	30	1.2	131.2
52	520	1.0	30	1.2	134.0
53	530	1.0	30	1.2	136.8
54	540	1.0	30	1.2	139.5
55	550	1.0	30	1.2	142.2
56	560	1.0	30	1.2	145.0
57	570	1.0	30	1.2	147.8
58	580	1.0	30	1.2	150.5
59	590	1.0	30	1.2	153.2
60	600	1.0	30	1.2	156.0
61	610	1.0	30	1.2	158.8
62	620	1.0	30	1.2	161.5
63	630	1.0	30	1.2	164.2
64	640	1.0	30	1.2	167.0
65	650	1.0	30	1.2	169.8
66	660	1.0	30	1.2	172.5
67	670	1.0	30	1.2	175.2

XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX L1 Y, Ruben SM;
XX
XX WPI: 1999-034722/03.
XX N-PSDB: AAV69760.
XX
XX
XX New isolated human G-protein coupled receptors - used to develop
XX products for treating e.g. asthma, Parkinson's disease, heart
XX failure, osteoporosis, hypertension, psychoses, eating disorders or
XX cancers
XX
XX Claim 1; Fig 1A-C; 65pp; English.
XX
XX This represents a EBV-induced G-protein coupled receptor (EBI-2)
XX polypeptide. The encoding DNA is deposited under the accession number
XX ATCC No: 209003. The invention provides two human G-protein coupled
XX receptor polypeptides. The polypeptides are human Epstein-Barr Virus
XX (EBV)-induced G-protein coupled receptor, designated EBI-2 polypeptide
XX and a human endothelium-differentiation gene (EDG) like G-protein coupled
XX receptor, designated EDG-1-like G-protein coupled receptor. Vectors
XX comprising the EBI-2 and EDG-1-like polypeptides encoding DNA can be used
XX to transform host cells for the recombinant production of the proteins.
XX Agonists for G-protein coupled receptors can be used for the treatment of
XX asthma, Parkinson's disease, acute heart failure, hypertension, urinary
XX retention and osteoporosis. Antagonists can be used for the treatment of
XX hypertension, angina pectoris, myocardial infarction, ulcers, asthma,
XX allergies, psychoses, depression, migraine, vomiting, stroke, eating
XX disorders, migraine headaches, cancer and benign prostatic hypertrophy.
XX The products can also be used for detection, diagnosis and drug
XX screening.
XX
XX Sequence 342 AA;
SQ
Query Match 100.0%; Score 1778; DB 20; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAVDNLTSAPGNTSLCTRDYKITQVLEPFLTYVLFVGLITNGLAMRIFPOIRSKSNFI 60
DB 1 MQAVDNLTSAPGNTSLCTRDYKITQVLEPFLTYVLFVGLITNGLAMRIFPOIRSKSNFI 60
QY 61 IELNNTVSDMLITPFEKILSDAKLGTGRLTFVQVSVITFYFYISISLGLITI 120
DB 61 IELNNTVSDMLITPFEKILSDAKLGTGRLTFVQVSVITFYFYISISLGLITI 120
QY 121 DRYOKTTRPEKTSNPKNLGAKILSVIWMFMFLSLPMLITNROPDKNVKCSFLKS 180
DB 121 DRYOKTTRPEKTSNPKNLGAKILSVIWMFMFLSLPMLITNROPDKNVKCSFLKS 180
QY 181 EFGLVMEIIVNYICQVIFWNIIFLIIVCYTLITRELYRSYVTRGVGKVRPKKYNVYFI 240
DB 181 EFGLVMEIIVNYICQVIFWNIIFLIIVCYTLITRELYRSYVTRGVGKVRPKKYNVYFI 240
QY 241 IIAVFETCFVHFARIPYITLSOTRDVFDCAENTLFFVKSTIMLTSLNACDPEYTF 300
DB 241 IIAVFETCFVHFARIPYITLSOTRDVFDCAENTLFFVKSTIMLTSLNACDPEYTF 300
QY 301 LCKSFRLNLSMLKCPNSATSLSDNRKREODGDPNEETPM 342
DB 301 LCKSFRLNLSMLKCPNSATSLSDNRKREODGDPNEETPM 342
RESULT 2
AAV71306
ID AAV71306 standard; Protein; 342 AA.
XX
AC AAV71306;
XX
DT 02-NOV-2000 (first entry)
XX
DE Human orphan G protein-coupled receptor hCHN8.

XX
XX Human; orphan G protein-coupled receptor; GPCR; hCHN8; drug screening;
XX transmembrane receptor; expressed sequence tag; EST; signal cascade.
XX
XX Homo sapiens.
XX
XX W0200031258-A2.
XX
XX
XX 02-JUN-2000.
XX
XX
XX 13-OCT-1999; 99WO-US23687.
XX
XX
XX 20-NOV-1998; 98US-0109213.
XX 16-FEB-1999; 99US-0120416.
XX 26-FEB-1999; 99US-0121852.
XX 12-MAR-1999; 99US-0123946.
XX 12-MAR-1999; 99US-0123949.
XX 28-MAY-1999; 99US-0136436.
XX 28-MAY-1999; 99US-0136437.
XX 28-MAY-1999; 99US-0136439.
XX 28-MAY-1999; 99US-0136567.
XX 28-MAY-1999; 99US-0137127.
XX 28-MAY-1999; 99US-0137131.
XX 29-JUN-1999; 99US-0141448.
XX 29-SEP-1999; 99US-0156555.
XX 29-SEP-1999; 99US-0156557.
XX 29-SEP-1999; 99US-0156633.
XX 29-SEP-1999; 99US-0156653.
XX 01-OCT-1999; 99US-0157280.
XX 01-OCT-1999; 99US-0157281.
XX 01-OCT-1999; 99US-0157282.
XX 01-OCT-1999; 99US-0157293.
XX 01-OCT-1999; 99US-0157294.
XX 12-OCT-1999; 99US-0416760.
XX 12-OCT-1999; 99US-0417044.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Chen R, Dang HT, Llaw CW, Lin I;
XX
XX WPI: 2000-400068/34.
XX N-PSDB: AAD01133.
XX
XX
XX Novel human orphan G protein-coupled receptors and the encoding cDNAs
XX for use in the identification of G protein-coupled receptor agonists -
XX
XX Claim 62; Page 82-83; 102pp; English.
XX
XX
XX The present amino acid sequence is the hCHN8, an endogenous human
XX orphan G protein-coupled receptor (GPCR), expressed in left and right
XX cerebellum, kidney and lung. The hCHN8 cDNA was identified using full
XX length EST (expressed sequence tag) 764455 as a probe.
XX The orphan GPCR of the invention, like all GPCRs has seven transmembrane
XX alpha helices with an extracellular N-terminus and an intracellular
XX C-terminus. However, no endogenous ligands has yet been identified for
XX the proteins of the invention. The orphan GPCRs may be used in the
XX identification of their endogenous ligands, and to screen potential GPCR
XX agonists and antagonists for use as pharmaceutical agents. The proteins
XX may also be used in the study of GPCR-mediated signalling cascades, and
XX to elucidate their precise role in normal and diseased human conditions.
XX Nucleic acid encoding human orphan GPCRs may be used for tissue
XX localisation expression analysis to provide information about their
XX function in healthy and pathological states.
XX
XX
SQ Sequence 342 AA;
Query Match 100.0%; Score 1778; DB 21; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAVDNLTSAPGNTSLCTRDYKITQVLEPFLTYVLFVGLITNGLAMRIFPOIRSKSNFI 60
DB 1 MQAVDNLTSAPGNTSLCTRDYKITQVLEPFLTYVLFVGLITNGLAMRIFPOIRSKSNFI 60

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QY 61 IFLNNTVISDLMLITPEPKILSDAKLGTGPLRTFVCQVTSVIFFTWYISISFLGLITI 120
DB 61 IFLNNTVISDLMLITPEPKILSDAKLGTGPLRTFVCQVTSVIFFTWYISISFLGLITI 120
QY 121 DRYOXTTRPEKTSNPKNLGAKILSVYIWMAPFLLSLPNMILTRNRPDRKVKKCSFLKS 180
DB 121 DRYOXTTRPEKTSNPKNLGAKILSVYIWMAPFLLSLPNMILTRNRPDRKVKKCSFLKS 180
QY 181 EFGIWMHEIVNYICQVIFWIMFLIVCYTLITKELYSYRTGCVGKVPKKVNVKVEI 240
DB 181 EFGIWMHEIVNYICQVIFWIMFLIVCYTLITKELYSYRTGCVGKVPKKVNVKVEI 240
QY 241 IIAVFICFVFPFHARIPYTLISQTRDVFDCYAEWTLFVYKKESTLMLSLNACLDPEIFYFF 300
DB 241 IIAVFICFVFPFHARIPYTLISQTRDVFDCYAEWTLFVYKKESTLMLSLNACLDPEIFYFF 300
QY 301 LCKSFNRLISMLKCPNSATSLSDNRRKKEDGDDPNEETPM 342
DB 301 LCKSFNRLISMLKCPNSATSLSDNRRKKEDGDDPNEETPM 342

RESULT 3
AAB02840
ID AAB02840 standard; Protein: 342 AA.
XX
AC AAB02840;
XX
DT 22-AUG-2000 (first entry)
XX
DE Human G protein coupled receptor hCHN8 protein SEQ ID NO:34.
XX
KM Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical;
KW mutant.
XX
OS Homo sapiens.
XX
PN WO200022131-A2.
XX
PD 20-Apr-2000.
XX
PF 13-OCT-1999; 99WO-US24065.
XX
PR 13-OCT-1998; 98US-0170496.
PR 12-NOV-1998; 98US-0108029.
PR 20-NOV-1998; 98US-0109213.
PR 27-NOV-1998; 98US-0110060.
PR 16-FEB-1999; 99US-0120416.
PR 26-FEB-1999; 99US-0121852.
PR 12-MAR-1999; 99US-0123944.
PR 12-MAR-1999; 99US-0123945.
PR 12-MAR-1999; 99US-0123946.
PR 12-MAR-1999; 99US-0123948.
PR 12-MAR-1999; 99US-0123949.
PR 12-MAR-1999; 99US-0123951.
PR 28-MAY-1999; 99US-0136436.
PR 28-MAY-1999; 99US-0136437.
PR 28-MAY-1999; 99US-0136439.
PR 28-MAY-1999; 99US-0136439.
PR 28-MAY-1999; 99US-0137127.
PR 28-MAY-1999; 99US-0137131.
PR 30-JUN-1999; 99US-0137567.
PR 27-AUG-1999; 99US-0141448.
PR 03-SEP-1999; 99US-0152524.
PR 29-SEP-1999; 99US-0156633.
PR 29-SEP-1999; 99US-0156535.
PR 29-SEP-1999; 99US-0156634.
XX
XX (AREN-) ARENA PHARM INC.
XX
PI Behan DP, Lehmann-Brulinsma K, Chalmers DT, Chen R, Dang HT;
Gore M, Liaw CW, Lin I, Lowitz K, White C;

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XX WPI: 2000-317986/27.
DR N-PSDB: AAA46034.
XX
PT Non-endogenous, human G protein-coupled receptors for screening
PT receptor, inverse or partial agonists useful as therapeutic agents
XX
PS Example 1; Page 112-113; 187pp; English.
XX
CC The present invention describes transmembrane receptors, preferably
CC human G protein coupled receptors (GPCR), for which the endogenous
CC ligand is unknown (Orphan GPCR receptors). More specifically the present
CC invention relates to non-endogenous, constitutively activated versions
CC of a human GPCR. These non-endogenous human GPCRs can be useful for
CC the direct identification of candidate compounds as receptor agonists,
CC inverse agonists or partial agonists for use as pharmaceutical agents.
CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
CC the exemplification of the present invention.
XX
SQ Sequence 342 AA;

Query Match 100.0%; Score 1778; DB 21; Length 342;
Best Local Similarity 100.0%; Pred. No. 3e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVDNILTSAPGNTSLCTRDYKITQVLPFLTYVLFVGLITNGIARIRFOIRSKSNFI 60
DB 1 MQAVDNILTSAPGNTSLCTRDYKITQVLPFLTYVLFVGLITNGIARIRFOIRSKSNFI 60
QY 61 IFLNNTVISDLMLITPEPKILSDAKLGTGPLRTFVCQVTSVIFFTWYISISFLGLITI 120
DB 61 IFLNNTVISDLMLITPEPKILSDAKLGTGPLRTFVCQVTSVIFFTWYISISFLGLITI 120
QY 121 DRYOXTTRPEKTSNPKNLGAKILSVYIWMAPFLLSLPNMILTRNRPDRKVKKCSFLKS 180
DB 121 DRYOXTTRPEKTSNPKNLGAKILSVYIWMAPFLLSLPNMILTRNRPDRKVKKCSFLKS 180
QY 181 EFGIWMHEIVNYICQVIFWIMFLIVCYTLITKELYSYRTGCVGKVPKKVNVKVEI 240
DB 181 EFGIWMHEIVNYICQVIFWIMFLIVCYTLITKELYSYRTGCVGKVPKKVNVKVEI 240
QY 241 IIAVFICFVFPFHARIPYTLISQTRDVFDCYAEWTLFVYKKESTLMLSLNACLDPEIFYFF 300
DB 241 IIAVFICFVFPFHARIPYTLISQTRDVFDCYAEWTLFVYKKESTLMLSLNACLDPEIFYFF 300
QY 301 LCKSFNRLISMLKCPNSATSLSDNRRKKEDGDDPNEETPM 342
DB 301 LCKSFNRLISMLKCPNSATSLSDNRRKKEDGDDPNEETPM 342

RESULT 4
AA94444
ID AA94444 standard; Protein: 342 AA.
XX
AC AA94444;
XX
DT 21-AUG-2000 (first entry)
XX
DE Human 15625 receptor protein.
XX
KW Human; G-protein-coupled receptor; GPCR; 15625 receptor protein;
KW glial cells; spleen; colon; liver; brain; T-cell; heart;
KW red cell; thymus; B-cell; pancreas; disorder; chromosome 3;
KW anaemia; neutropenia; thrombocytopenia; gene therapy; ss.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FT Domain 1..25
XX FT Modified-site /label= extracellular_domain
XX FT Misc-difference 6..9 /label= N-glycosylation
XX FT Misc-difference 13

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FT Modified-site /note- "encoded by ACC"
FT 13..16 /label= N-glycosylation
FT Domain /label= Transmembrane_domain
FT 26..302 /label= N-myristoylation
FT Modified-site 39..44
FT 121..123 /label= GPCR signal transduction site
FT Modified-site 126..128 /label= protein_kinase_C_phosphorylation
FT Modified-site 163..165 /label= protein_kinase_C_phosphorylation
FT Modified-site 173..176 /label= protein_kinase_phosphorylation
FT Domain 303..342 /label= Intracellular_domain
FT Modified-site 304..306 /label= protein_kinase_C_phosphorylation
FT Modified-site 333..338 /label= N-myristoylation
FT Modified-site /label= N-myristoylation
FT WO200028028-A1.
FT 18-MAY-2000.
FT 05-NOV-1999; 99WO-US25956.
FT 06-NOV-1998; 98US-0187134.
FT 25-AUG-1999; 99US-0382918.
FT (MILL-) MILLENNIUM PHARM INC.
FT Glucksman MA, Gu W, Welch NS;
FT WPI: 2000-376543/32.
FT N-PSDB; AAA27126.
FT Identifying an agent modulating the level or activity of G-protein
PT coupled receptor useful for screening a cell derived from a subject
PT having disorders such as anaemia, neutropenia and thrombocytopenia
PS Disclosure: Page 88-89; 97pp; English.
PS
XX The present sequence shows the 15625 receptor protein. It is a novel
XX G-coupled protein receptor (GPCR). The cDNA for this protein was
XX isolated by screening a human cDNA library with sequences homologous
XX to other GPCRs. The 15625 receptor protein is expressed in the glial
XX cells of the brain. It is also expressed in several other tissues.
XX The 15625 receptor protein may be useful for producing antibodies
XX which can be used to detect the presence of the receptor protein.
XX The 15625 receptor protein polynucleotides are useful for generating
XX probes, primers and antisense constructs. The polynucleotides
XX encoding the 15625 receptor proteins can also be inserted into
XX vectors to be used in gene therapy. The disorder that may be treated
XX using the 15625 receptor protein polynucleotides and polypeptides
XX include anaemia, neutropenia and thrombocytopenia.
XX
SQ Sequence 342 AA:
Query Match 100.0%; Score 1778; DB 21; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAVDNLTSAAGNTSLCTRDYKITQVLEPLLYTLFVGLITNGLAMRIFQIRKSNFI 60
DB 1 MQAVDNLTSAAGNTSLCTRDYKITQVLEPLLYTLFVGLITNGLAMRIFQIRKSNFI 60
QY 61 IFLKNTYISDLMLTPEPKILSDAKLGTPFVCOVTSVIFPMYISISFLGLITI 120
DB 61 IFLKNTYISDLMLTPEPKILSDAKLGTPFVCOVTSVIFPMYISISFLGLITI 120
QY 121 DRYOKTRPFTKSNPKMLGAKILSVIWMFMLISLPNMLITNRPDRKNVKKCSFLKS 180

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DB 121 DRYOKTRPFTKSNPKMLGAKILSVIWMFMLISLPNMLITNRPDRKNVKKCSFLKS 180
QY 181 EFGLVHWEIYNYICQVLFWMINFLIVICYTLITREKRSVTRGVGKVPKKVNVVFI 240
DB 181 EFGLVHWEIYNYICQVLFWMINFLIVICYTLITREKRSVTRGVGKVPKKVNVVFI 240
QY 241 IIAVFICFVPEFHARIPYTLISQTRDVFDCYAEFTLEFYVESTLMTSLNACDPEFYFF 300
DB 241 IIAVFICFVPEFHARIPYTLISQTRDVFDCYAEFTLEFYVESTLMTSLNACDPEFYFF 300
QY 301 LCSFRNSLISMLKCPNSATSLSDNKKRKGDDGDPNEETPM 342
DB 301 LCSFRNSLISMLKCPNSATSLSDNKKRKGDDGDPNEETPM 342
RESULT 5
ID AAM79249 standard; Protein: 342 AA.
AC AAM79249;
DT 06-NOV-2001 (first entry)
DE Human protein SEQ ID NO 1911.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation.
XX
XX Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US04098.
XX
XX 03-FEB-2000; 2000US-0496914.
XX 27-APR-2000; 2000US-0560875.
XX 20-JUN-2000; 2000US-0598075.
XX 19-JUL-2000; 2000US-0620325.
XX 01-SEP-2000; 2000US-0654936.
XX 15-SEP-2000; 2000US-0663561.
XX 20-OCT-2000; 2000US-0693325.
XX 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
XX Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
XX N-PSDB; AAK52382.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 4310; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activity/inhbin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.

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CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.

SO Sequence 342 AA;

Query Match 100.0%; Score 1778; DB 22; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MOAVDNLSAPGNTSLCTRDYKITQVLPPLTYVLFVGLITNGLAMRIFQIRKSNFI 60
DB 1 MOAVDNLSAPGNTSLCTRDYKITQVLPPLTYVLFVGLITNGLAMRIFQIRKSNFI 60
OY 61 IFLKMTVSDLMILTFPFKILSDAKLGTGRLTFVCOVTSVIEFTWYISISFGLITI 120
DB 61 IFLKMTVSDLMILTFPFKILSDAKLGTGRLTFVCOVTSVIEFTWYISISFGLITI 120
OY 121 DRYQKTTTPFKTSNPKNLGAKILSVIWAEMFELSLPMILITNQPDKNVKCSFLKS 180
DB 121 DRYQKTTTPFKTSNPKNLGAKILSVIWAEMFELSLPMILITNQPDKNVKCSFLKS 180
OY 181 EFGVWHEIVNYICGVIFWINEFLIVCYTLITKELYSYVTRGVGKVPKKVAVKFI 240
DB 181 EFGVWHEIVNYICGVIFWINEFLIVCYTLITKELYSYVTRGVGKVPKKVAVKFI 240
OY 241 IIAVFICFVPPHFAIRIYITLSQTRDVDCFAENTLFFVKESTLWLTSLNCLDPFIYFF 300
DB 241 IIAVFICFVPPHFAIRIYITLSQTRDVDCFAENTLFFVKESTLWLTSLNCLDPFIYFF 300
OY 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEDGDPNEETPM 342
DB 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEDGDPNEETPM 342

RESULT 6
AAE04386
ID AAE04386 standard; Protein; 342 AA.
XX
AC AAE04386;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human P2-purinegic receptor subtype, P2Y12.
XX
KW Human; P2-purinegic receptor; P2Y12; cardiant; vasotrophic; thrombolytic; cerebroprotective; gynecological; ADP; adenosine 5'-diphosphate; angina; myocardial infarction; ischaemic attack; pre-eclampsia; bleeding disorder; carotid endarterectomy; vascular graft surgery; brain disorder; migraine; vascular injury; schizophrenia; eating disorder; depression; angiodysplasia; peripheral vascular disease; platelet aggregation; restenotic; embolism; thrombocytopenic purpura; stroke; pertussis toxin-sensitive G protein; GI; disseminated intravascular coagulation; thrombosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 27..50 /label= Transmembrane_domain_1
FT /label= Transmembrane_domain_1
FT 58..82 /label= Transmembrane_domain_2
FT /label= Transmembrane_domain_2
FT 97..121 /label= Transmembrane_domain_3
FT /label= Transmembrane_domain_3
FT 140..163 /label= Transmembrane_domain_4
FT /label= Transmembrane_domain_4
FT 189..213 /label= Transmembrane_domain_5
FT /label= Transmembrane_domain_5
FT 234..259 /label= Transmembrane_domain_6
FT /label= Transmembrane_domain_6
FT 278..303 /label= Transmembrane_domain_7
FT /label= Transmembrane_domain_7
XX
PN WO200146454-A1.

XX 28-JUN-2001.
PD 26-DEC-2000; 2000WO-US34998.
XX
PF 26-DEC-2000; 2000WO-US34998.
XX
PR 23-DEC-1999; 99US-0171622.
XX
PA (COR-) COR THERAPEUTICS INC.
PI Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;
PI Holoopeter G;
XX WPI: 2001-418082/44.
DR N-PSDB: AAD08695.
XX
PT Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful
PT for identifying binding partners and for diagnostic applications -
XX
PS Example 1; Fig 5A; 108bp; English.
XX
CC The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed
CC as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is
CC the subtype of P2-purinegic receptor. The P2Y12 receptor is expressed
CC selectively in the platelets and brain, and couples to a pertussis toxin-
CC sensitive G protein (G_i). P2Y12 receptor is a G protein-coupled receptor
CC that responds to ADP. The invention also relates to a method for
CC identifying an agent which is useful for modulating acute myocardial
CC infarction, unstable angina, chronic stable angina, transient ischaemic
CC attacks, strokes, peripheral vascular disease, pre-eclampsia, deep venous
CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic
CC thrombocytopenic purpura or a bleeding disorder; carotid endarterectomy,
CC restenotic complications following angioplasty, carotid endarterectomy,
CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery,
CC stent placements or insertion of endovascular devices and prostheses.
CC P2Y12 receptor is useful for identifying binding partners and for
CC diagnostic applications. P2Y12 receptor provides targets for screening
CC synthetic small molecules and combinatorial or naturally occurring
CC compound libraries to regulate platelet aggregation, vascular injury, or
CC disease as well as schizophrenia, eating disorders, depression, migraine
CC and other brain disorders. The present sequence is human P2-purinegic
CC receptor subtype, referred as P2Y12.
XX
SQ Sequence 342 AA;
XX
Query Match 100.0%; Score 1778; DB 22; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MOAVDNLSAPGNTSLCTRDYKITQVLPPLTYVLFVGLITNGLAMRIFQIRKSNFI 60
DB 1 MOAVDNLSAPGNTSLCTRDYKITQVLPPLTYVLFVGLITNGLAMRIFQIRKSNFI 60
OY 61 IFLKMTVSDLMILTFPFKILSDAKLGTGRLTFVCOVTSVIEFTWYISISFGLITI 120
DB 61 IFLKMTVSDLMILTFPFKILSDAKLGTGRLTFVCOVTSVIEFTWYISISFGLITI 120
OY 121 DRYQKTTTPFKTSNPKNLGAKILSVIWAEMFELSLPMILITNQPDKNVKCSFLKS 180
DB 121 DRYQKTTTPFKTSNPKNLGAKILSVIWAEMFELSLPMILITNQPDKNVKCSFLKS 180
OY 181 EFGVWHEIVNYICGVIFWINEFLIVCYTLITKELYSYVTRGVGKVPKKVAVKFI 240
DB 181 EFGVWHEIVNYICGVIFWINEFLIVCYTLITKELYSYVTRGVGKVPKKVAVKFI 240
OY 241 IIAVFICFVPPHFAIRIYITLSQTRDVDCFAENTLFFVKESTLWLTSLNCLDPFIYFF 300
DB 241 IIAVFICFVPPHFAIRIYITLSQTRDVDCFAENTLFFVKESTLWLTSLNCLDPFIYFF 300
OY 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEDGDPNEETPM 342
DB 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEDGDPNEETPM 342

RESULT 7

AB077868 standard; Protein; 342 AA.

ID ABB77868;

XX ABB77868;

DT 27-SEP-2002 (first entry)

XX Amino acid sequence of human ADP receptor P2YAC protein.

KW Human; ADP receptor; P2YAC; antiplatelet agent; thrombotic disease;

XX ischaemic disease.

XX Homo sapiens.

XX WO200236631-A1.

XX 10-MAY-2002.

XX 31-OCT-2001; 2001WO-JP09534.

XX 01-NOV-2000; 2000JP-0334721.

XX 11-JAN-2001; 2001JP-0003577.

XX (YAMA) YAMANOUCHI PHARM CO LTD.

XX Takasaki J, Matsumoto M, Kamohara M, Saito T, Ohishi T, Soga T;

XX WPI: 2002-519236/55.

XX N-PSDB; ABL59205.

XX Method for screening anti-platelet agents with human ADP receptor P2YAC

XX protein, its functional equivalent, or its homologous protein, as tool,

XX for treating e.g. thrombotic or ischaemic diseases.

XX Claim 1; Page 48-49; 56pp; Japanese.

XX The present sequence represents a human ADP receptor P2YAC protein. It is

XX used as a screening tool for screening for antiplatelet agents. The

XX method is used for screening for antiplatelet agents, which can then

XX be used for treating e.g. thrombotic or ischaemic diseases.

XX Sequence 342 AA;

XX Query Match 100.0%; Score 1778; DB 23; Length 342;

XX Best Local Similarity 100.0%; Pred. No. 5e-187;

XX Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 MOAVDNLTSAGNNTSLCRODKITQVLEPLLYTLFVGLITNGLAMRIFQIRSKSNEI 60

XX 1 MOAVDNLTSAGNNTSLCRODKITQVLEPLLYTLFVGLITNGLAMRIFQIRSKSNEI 60

XX 61 IFLKNTYISDLMLTPEPKILSDAKLGTPLRFTVCVSVIFETWYISISFGLITI 120

XX 61 IFLKNTYISDLMLTPEPKILSDAKLGTPLRFTVCVSVIFETWYISISFGLITI 120

XX 121 DRYKTRPFTSPKNIKAKIISVYIWMFPLSLPMLTNRQPRDKVKKCSPLKS 180

XX 121 DRYKTRPFTSPKNIKAKIISVYIWMFPLSLPMLTNRQPRDKVKKCSPLKS 180

XX 181 EFLGWHMEIYVICQVFMIFELIVICYTLITKEIYRSYRTGCVGVPRKKVAKVEI 240

XX 181 EFLGWHMEIYVICQVFMIFELIVICYTLITKEIYRSYRTGCVGVPRKKVAKVEI 240

XX 241 IIAVFICFVPHFARIPYTLISQTRDVFDCYAEMLTFYVKESTLMTLSLNACLDPEITFF 300

XX 241 IIAVFICFVPHFARIPYTLISQTRDVFDCYAEMLTFYVKESTLMTLSLNACLDPEITFF 300

XX 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEDGDDPNEETPM 342

XX 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEDGDDPNEETPM 342

RESULT 8

AA080164 standard; Protein; 342 AA.

ID AA080164;

XX AA080164;

DT 15-JUL-2002 (first entry)

XX Human ADP-glucose receptor.

KW Human; ADP-glucose; receptor; G protein-coupled receptor;

KW agonist; antagonist; cardiovascular function disorder; vasorelaxation;

KW ischaemia; angina pectoris; gastrointestinal disorder; diarrhoea;

KW immune disorder; immunodeficiency disorder; autoimmune disorder;

KW rheumatoid arthritis; bacterial infection; viral infection;

KW fungal infection; protozoal infection; respiratory disorder; asthma;

KW kidney disorder; glomerulonephritis; hepatobiliary disorder; cirrhosis;

KW endocrine disorder; adrenal dysfunction; musculoskeletal disorder;

KW osteoporosis; nervous system disorder; Alzheimer's disease;

KW psychotic disorder; depression; cancer; pain; glycogen storage disease;

KW disorder of body weight; AIDS; acquired immunodeficiency syndrome;

XX chromosome 3; Usher's syndrome, type 3.

XX Homo sapiens.

XX WO200224942-A2.

XX 28-MAR-2002.

XX 19-SEP-2001; 2001WO-US29523.

XX 20-SEP-2000; 2000US-234023P.

XX 09-FEB-2001; 2001US-0780576.

XX (REGC) UNIV CALIFORNIA.

XX Clivelli O, Notackner H, Wang Z, Reinscheid R;

XX WPI: 2002-383195/41.

XX N-PSDB; ABK50286.

XX Identifying an agonist, antagonist or ligand of an ADP-glucose

XX receptor, for treating cardiovascular, gastrointestinal, kidney,

XX endocrine, immune disorders, and bacterial, viral, protozoal or fungal

XX infections.

XX Claim 3; Fig 1; 86pp; English.

XX The invention relates to identifying an ADP-glucose (ADP-G) receptor (a

XX G protein-coupled receptor) agonist, antagonist or ligand, comprises

XX contacting the receptor with one or more candidate compounds so that the

XX receptor produces a G protein-coupled signal in response to ADP-G or

XX selectively binds ADP-G, and identifying the candidate molecule that

XX alters signal production as an agonist, antagonist or binds as a ligand.

XX Also included are altering signalling through an ADP-G receptor, by

XX contacting a cell expressing the receptor with ADP-G or the anti/agonist,

XX ameliorating an ADP-G receptor associated condition, by administering a

XX therapeutic composition comprising ADP-G or the anti/agonist to an

XX individual and a composition comprising the ADP-G receptor and ADP-G.

XX ADP-G or the anti/agonist is useful for treating an ADP-G receptor

XX associated condition e.g. cardiovascular function disorder, where the

XX therapeutic composition induces vasorelaxation. The new methods are

XX useful in identifying anti/agonists and ligands of the receptor.

XX The anti/agonists are useful therapeutically for preventing or

XX ameliorating conditions associated with the receptor such as

XX cardiovascular disorders (e.g. ischaemia, hypertension, hypotension,

XX angina pectoris, myocardial infarction, stroke, congestive heart

XX failure, shock, erectile dysfunction, orthostatic intolerance and

XX migraine), gastrointestinal disorders (e.g. diarrhoea, gastritis,

XX inflammatory bowel disease), immune disorders (e.g. immunodeficiency

XX disorders, autoimmune disorders, rheumatoid arthritis), infections

XX caused by bacteria, fungi, protozoa or virus, respiratory disorders

XX (e.g. asthma, pneumonia, bronchitis), kidney disorders (e.g.

CC glomerulonephritis, renal failure, lupus), hepatobiliary disorders
CC (e.g. jaundice, cirrhosis, hepatitis), endocrine disorders (e.g.
CC pituitary, thyroid or adrenal dysfunctions), musculoskeletal disorders
CC (e.g. osteoporosis, muscular dystrophies), nervous system disorders
CC (e.g. Parkinson's and Alzheimer's disease), psychotic disorders (e.g.
CC depression, anxiety, schizophrenia), pain, glycogen storage
CC diseases and disorders of body weight (e.g. as a result of cancer
CC or AIDS, acquired immunodeficiency syndrome). The gene for the ADP-G
CC receptor is located on chromosome 3 in a region associated with Usher
CC syndrome type 3 (progressive hearing loss). The ligand is useful
CC therapeutically, in detecting normal or abnormal expression of the
CC receptor in an isolated sample or in in vivo diagnostic imaging
CC procedures, and targeting specifically a diagnostic group to cells and
CC tissues that express the receptor. The present sequence represents the
CC ADP-G receptor.
XX
XX

Sequence 342 AA:

Query Match 100.0%; Score 1778; DB 23; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOAVNLTSAPENTSLCTRDYKITQVLPFLTYVLFVGLITNGLAMRIFFQIRKSNFI 60
DB 1 MOAVNLTSAPENTSLCTRDYKITQVLPFLTYVLFVGLITNGLAMRIFFQIRKSNFI 60
QY 61 IFLKNTVISDLMLITFPFKILSDAKLGTGRLTFVCOVTSVIFYFTWYISISFLGLITI 120
DB 61 IFLKNTVISDLMLITFPFKILSDAKLGTGRLTFVCOVTSVIFYFTWYISISFLGLITI 120
QY 121 DRYQKTRPRFKTSNPKNLGAKILSVIWAFFLISLPMILTNOPRDKNVKCSFLKS 180
DB 121 DRYQKTRPRFKTSNPKNLGAKILSVIWAFFLISLPMILTNOPRDKNVKCSFLKS 180
QY 181 EGGLEWHEIVNTICQVIFEMINFLIYVCYTLTKELYSYVTRGVGKPRKVVWVKYFI 240
DB 181 EGGLEWHEIVNTICQVIFEMINFLIYVCYTLTKELYSYVTRGVGKPRKVVWVKYFI 240
QY 241 IIAVEFICVPPHFAPIPTYSQTRDVEDCAENTLFFVKESTLWLTSLNACLDPIFYFF 300
DB 241 IIAVEFICVPPHFAPIPTYSQTRDVEDCAENTLFFVKESTLWLTSLNACLDPIFYFF 300
QY 301 ICKSFRNSLISMLKCPNSATSLSDNRKKEDGDPNNEETPM 342
DB 301 ICKSFRNSLISMLKCPNSATSLSDNRKKEDGDPNNEETPM 342

RESULT 9

AA048353
ID AA048353 standard; Protein: 342 AA.

AC AA048353;

DT 25-APR-2002 (first entry)

DE Human G protein-coupled receptor, IGPCR17.

XX Human: G protein-coupled receptor; IGPCR17; analgesic; neuroleptic;
XX trianquilliser; antiParkinsonian; neuroprotective; nootropic;
XX anticonvulsant; metabolic; anorectic; anabolic; antiinflammatory;
XX antidiabetic; osteopathic; antisthmatic; antiallergic; antiarthritic;
XX immunosuppressive; gene therapy; psychiatric disorder;
XX central nervous system disorder; movement dysfunction; schizophrenia;
XX multiple sclerosis; Alzheimer's disease; kidney disease; obesity;
XX gastrointestinal disorder; osteoporosis; infection;
XX gynecological disorder; receptor.

OS Homo sapiens.

XX WO200202599-A2.

XX 10-JAN-2002.

PF 02-JUL-2001; 2001WO-EP07532.

XX 30-JUN-2000; 2000US-215759P.

XX (INVE-) INGENIUM PHARM AG.

PI Wattler F, Wattler S, Trommler P, Nehls MC;

XX WPI: 2002-140080/18.

DR N-PSDB; ABA96535.

PT New human or mouse G protein-coupled receptor protein, IGPCR17, useful
PT for diagnosis, prevention, amelioration or treatment of central nervous
PT system disorders such as Tourette's syndrome, Parkinson's disease and
PT pain
XX
XX

PS Claim 8: Fig 2; 71pp: English.

XX The present sequence is the protein sequence for human G protein-coupled
CC receptor (GPCR) protein, IGPCR17. The coding sequence for IGPCR17 is
CC useful in gene therapy for prevention, amelioration or treatment of
CC diseases characterised by aberrant expression or activity of IGPCR17,
CC where the disease is a psychiatric or central nervous system (CNS)
CC disorder associated with signal processing in CNS such as learning and
CC memory disorders, movement dysfunctions, tics, tremor, Tourette's
CC syndrome, Parkinson's disease, Huntington's disease, dyskinesias,
CC dystonia, pain and spasms. In addition, IGPCR17 and its coding sequence
CC are useful in diagnosis, prevention, amelioration or treatment of
CC diseases associated with signal processing in CNS, schizophrenia,
CC episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive
CC disorder (OCD), multiple sclerosis, Alzheimer's disease/dementia,
CC anorexia, kidney diseases such as renal failure, obesity,
CC gastrointestinal disorders such as irritable bowel syndrome (IBS),
CC diarrhoea, motility disorders and conditions of delayed gastric emptying,
CC osteoporosis, infections such as bacterial, fungal, protozoal and viral
CC infections, asthma, allergy, arthritis, sepsis and gynecological
CC disorders.
XX

Sequence 342 AA:

Query Match 100.0%; Score 1778; DB 23; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOAVNLTSAPENTSLCTRDYKITQVLPFLTYVLFVGLITNGLAMRIFFQIRKSNFI 60
DB 1 MOAVNLTSAPENTSLCTRDYKITQVLPFLTYVLFVGLITNGLAMRIFFQIRKSNFI 60
QY 61 IFLKNTVISDLMLITFPFKILSDAKLGTGRLTFVCOVTSVIFYFTWYISISFLGLITI 120
DB 61 IFLKNTVISDLMLITFPFKILSDAKLGTGRLTFVCOVTSVIFYFTWYISISFLGLITI 120
QY 121 DRYQKTRPRFKTSNPKNLGAKILSVIWAFFLISLPMILTNOPRDKNVKCSFLKS 180
DB 121 DRYQKTRPRFKTSNPKNLGAKILSVIWAFFLISLPMILTNOPRDKNVKCSFLKS 180
QY 181 EGGLEWHEIVNTICQVIFEMINFLIYVCYTLTKELYSYVTRGVGKPRKVVWVKYFI 240
DB 181 EGGLEWHEIVNTICQVIFEMINFLIYVCYTLTKELYSYVTRGVGKPRKVVWVKYFI 240
QY 241 IIAVEFICVPPHFAPIPTYSQTRDVEDCAENTLFFVKESTLWLTSLNACLDPIFYFF 300
DB 241 IIAVEFICVPPHFAPIPTYSQTRDVEDCAENTLFFVKESTLWLTSLNACLDPIFYFF 300
QY 301 ICKSFRNSLISMLKCPNSATSLSDNRKKEDGDPNNEETPM 342
DB 301 ICKSFRNSLISMLKCPNSATSLSDNRKKEDGDPNNEETPM 342

RESULT 10

ABB05031
ID ABB05031 standard; Protein: 342 AA.

XX

AC ABB05031;
XX
DT 25-MAR-2002 (first entry)
XX
DE Human SP168 receptor protein SEQ ID NO:2.
XX
KW Human, SP168 receptor; mammalian G-protein coupled receptor; GPCR;
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
KW Huntington's disease; amyotrophic lateral sclerosis; ALS; MS; receptor;
KW multiple sclerosis.
XX
OS Homo sapiens.
XX
PN US2001046497-A1.
XX
PD 29-NOV-2001.
XX
PF 16-APR-2001; 2001US-0835922.
XX
PR 21-APR-2000; 2000US-199041P.
XX
PA (ZHANG/) ZHANG F L.
PA (LLOU/) LUO L.
PA (GUST/) GUSTAFSON E.
PA (LIU/) LIU Y.
PA (CHEN/) CHEN G.
XX
PI Zhang FL, Luo L, Gustafson E, Liu Y, Chen G;
XX
XX WPI: 2002-082414/11.
DR N-PSDB: ABA92641.
XX
PT Identifying modulators of mammalian G-Protein Coupled Receptor SP168,
PT useful for treating Parkinson's Disease, Alzheimer's Disease,
PT Huntington's Disease, amyotrophic lateral sclerosis and multiple
PT sclerosis -
XX
XX Claim 3; Page 14-15; 16pp; English.
XX
XX The present invention describes a method for identifying agonists and
XX antagonists of mammalian G-Protein Coupled Receptor (GPCR) SP168 which
XX may be used to treat neurodegenerative disorders. The method comprises:
XX (a) contacting a mammalian SP168 receptor (or a functional fragment) in
XX the presence of a known amount of a labeled SP168 receptor ligand with
XX a sample to be tested for the presence of the SP168 receptor agonist or
XX antagonist; and (b) measuring the amount of labeled SP168 ligand
XX specifically bound to the receptor (the SP168 receptor agonist or
XX antagonist in the sample is identified by measuring the difference in
XX binding of the labeled SP168 receptor ligand to the receptor, compared
XX to what would be measured in the absence of such agonist or antagonist).
XX The method is used to detect agonists and antagonists (especially
XX antibodies) of the SP168 GPCR which may be used to treat a
XX neurodegenerative disorder, such as Parkinson's Disease, Alzheimer's
XX Disease, Huntington's Disease, amyotrophic lateral sclerosis (ALS) and
XX multiple sclerosis (MS) in mammals, especially humans. The present
XX sequence represents the human SP168 receptor which can be used in the
XX method of the invention.
XX
SQ Sequence 342 AA;
Query Match 100.0%; Score 1778; DB 23; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MQAVDNLTSAAGNTSLCTRDYKITQVLEPLLYTVLFEVGLITNGIAMRIFFOIRSKSNFI 60
DB 1 MQAVDNLTSAAGNTSLCTRDYKITQVLEPLLYTVLFEVGLITNGIAMRIFFOIRSKSNFI 60
OY 61 IFLKNTVTSIDLLMTLTFEFKILSDAKLGTGRLRTFVCCVTSVIFFTYIISIFGLITTI 120
DB 61 IFLKNTVTSIDLLMTLTFEFKILSDAKLGTGRLRTFVCCVTSVIFFTYIISIFGLITTI 120
OY 121 DRYOKTRPFKTSNPKNLGAKILSVIWMFLLSLPNNMLITNRQPRDKNVKCSFLKS 180

DB 121 DRYOKTRPFKTSNPKNLGAKILSVIWMFLLSLPNNMLITNRQPRDKNVKCSFLKS 180
OY 181 EFGLVWHEIVNYICOVIPWINEFLIYVCYTLITELVRSYRFGVGVPRKYNVAFI 240
DB 181 EFGLVWHEIVNYICOVIPWINEFLIYVCYTLITELVRSYRFGVGVPRKYNVAFI 240
OY 241 IIAVEFICFVPHFARIPYTLISQTRDVEDCTAENTLFPYKRESTMNLNACLDPIYFF 300
DB 241 IIAVEFICFVPHFARIPYTLISQTRDVEDCTAENTLFPYKRESTMNLNACLDPIYFF 300
OY 301 LCKSFRNLSIMLKCPNATSLSDNRRKKEDGCDPNEETPM 342
DB 301 LCKSFRNLSIMLKCPNATSLSDNRRKKEDGCDPNEETPM 342
RESULT 11
AAG80236
ID AAG80236 standard; Protein; 342 AA.
XX
AC AAG80236;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human PAFR3 protein.
XX
KW PAFR-3; platelet activating factor receptor; human; chromosome 3;
KW thrombocyte activation; hypotension; vascular permeability;
KW bronchoconstriction; transgenic animal; knockout animal.
XX
XX Homo sapiens.
XX
XX DE10020073-A1.
XX
XX 25-OC-2001.
XX
XX 22-APR-2000; 2000DE-1020073.
XX
XX 22-APR-2000; 2000DE-1020073.
XX
XX (BRUE/) BRUESS M.
XX (BOEN/) BOENISCH H.
XX
XX Bruess M, Boenisch H;
XX
XX WPI: 2002-027296/04.
XX
XX N-PSDB: AAI68802, AAI68803.
XX
XX New human platelet-activating factor (PAF) receptor-3 gene, useful for
XX diagnosis and treatment of PAF-related diseases -
XX
XX Disclosure; Page 4; 6pp; German.
XX
XX This invention describes a novel human platelet-activating factor (PAF)
XX receptor-3 (PAFR-3) gene (I). The protein encoded by (I) probably
XX modulates the activity of PAF, which is involved in many
XX (patho)physiological processes, e.g., thrombocyte activation,
XX hypotension, increased vascular permeability, bronchoconstriction etc.
XX (I), and derived (anti)sense oligonucleotides, are useful in the
XX treatment and diagnosis of (I)-related diseases; for producing
XX transgenic/knockout animals, and for recombinant expression of the
XX protein (II) that it encodes. (II) is useful in ligand-binding studies
XX and screening assays, also for treatment and diagnosis of (II)-related
XX diseases. This sequence represents the human platelet-activating
XX factor receptor (PAFR-3) protein described in the invention.
XX
SQ Sequence 342 AA;
Query Match 100.0%; Score 1778; DB 23; Length 342;
Best Local Similarity 100.0%; Pred. No. 5e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MQAVDNLTSAAGNTSLCTRDYKITQVLEPLLYTVLFEVGLITNGIAMRIFFOIRSKSNFI 60

```

|||||
Db 1 MQAVDNLTSAGNTSLCTRDYKITQVLEPPLYTVLFFVGLITNGLAMKIFQIRKSNFI 60
QY 61 IFLKNTVSDLLMLITFPFKILSDAKLGTGDLRTFVCQVTSVIFFTWYISISFGLITI 120
Db 61 IFLKNTVSDLLMLITFPFKILSDAKLGTGDLRTFVCQVTSVIFFTWYISISFGLITI 120
QY 121 DRYKTRPFTSNPKNLGAKILSVIWMFLLSLPNMILTNRPDKNVKCSFLKS 180
Db 121 DRYKTRPFTSNPKNLGAKILSVIWMFLLSLPNMILTNRPDKNVKCSFLKS 180
QY 181 EFGVWHEIVNYICQVIFWINEFLIYVCYTLITKELYSYRTGCVGVPKKVNVKFI 240
Db 181 EFGVWHEIVNYICQVIFWINEFLIYVCYTLITKELYSYRTGCVGVPKKVNVKFI 240
QY 241 IIAVFICFVPHFARIPYTLISQTRDVFDCIAENTLFFVKESTLMLTSLNCLDPFIYFF 300
Db 241 IIAVFICFVPHFARIPYTLISQTRDVFDCIAENTLFFVKESTLMLTSLNCLDPFIYFF 300
QY 301 LCKSFNSLSMLKCPNSATSLSDNRRKKEDGDGDPNEETPM 342
Db 301 LCKSFNSLSMLKCPNSATSLSDNRRKKEDGDGDPNEETPM 342

RESULT 12
AAI94445
ID AAY94445 standard; Protein: 342 AA.
AC AAY94445;
XX
DN 21-AUG-2000 (first entry)
XX
DE Macaque ortholog of human 15625 receptor protein.
XX
KW Human; G-protein-coupled receptor; GPCR; 15625 receptor protein;
KW glial cells; spleen; colon; liver; brain; T-cell; heart;
KW red cell; thymus; B-cell; pancreas; disorder; chromosome 3;
KW anaemia; neutropenia; thrombocytopenia; gene therapy; ss.
XX
OS Macaca sp.
XX
PN WO200028028-A1.
PD 18-MAY-2000.
XX
PF 05-NOV-1999; 99WO-US25956.
XX
PR 06-NOV-1998; 98US-0187134.
PR 25-AUG-1999; 99US-0382918.
XX
PA (MILL-) MILLENNIUM PHARM INC.
PI Gluckemann MA, Gu W, Welch NS;
XX
DR WPI: 2000-376543/32.
DR N-PSDB: AAA27127.
XX
PT Identifying an agent modulating the level or activity of G-protein
PT coupled receptor useful for screening a cell derived from a subject
PT having disorders such as anaemia, neutropenia and thrombocytopenia
XX
PS Disclosure; Page 90-92; 97pp; English.
XX
CC The 15625 receptor protein is a novel G-coupled protein receptor (GPCR).
CC The cDNA for this protein was isolated by screening a human cDNA library
CC with sequences homologous to other GPCRs. The 15625 receptor protein is
CC expressed in the glial cells of the brain. It is also expressed in
CC several other tissues. The 15625 receptor protein may be useful for
CC producing antibodies which can be used to detect the presence of the
CC receptor protein. The 15625 receptor protein polynucleotides are useful
CC for generating probes, primers and antisense constructs. The
CC polynucleotides encoding the 15625 receptor proteins can also be inserted
CC into vectors to be used in gene therapy. The disorder that may be

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CC treated using the 15625 receptor protein polynucleotides and
CC polypeptides include anaemia, neutropenia and thrombocytopenia. The
CC present sequence is the macaque ortholog of the human 15625 receptor
CC protein.
XX
SQ Sequence 342 AA;
Query Match 98.3%; Score 1748; DB 21; Length 342;
Best Local Similarity 98.0%; Pred. No. 1e-183;
Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 MQAVDNLTSAGNTSLCTRDYKITQVLEPPLYTVLFFVGLITNGLAMKIFQIRKSNFI 60
Db 1 MQAVDNLTSAGNTSLCTRDYKITQVLEPPLYTVLFFVGLITNGLAMKIFQIRKSNFI 60
QY 61 IFLKNTVSDLLMLITFPFKILSDAKLGTGDLRTFVCQVTSVIFFTWYISISFGLITI 120
Db 61 IFLKNTVSDLLMLITFPFKILSDAKLGTGDLRTFVCQVTSVIFFTWYISISFGLITI 120
QY 121 DRYKTRPFTSNPKNLGAKILSVIWMFLLSLPNMILTNRPDKNVKCSFLKS 180
Db 121 DRYKTRPFTSNPKNLGAKILSVIWMFLLSLPNMILTNRPDKNVKCSFLKS 180
QY 181 EFGVWHEIVNYICQVIFWINEFLIYVCYTLITKELYSYRTGCVGVPKKVNVKFI 240
Db 181 EFGVWHEIVNYICQVIFWINEFLIYVCYTLITKELYSYRTGCVGVPKKVNVKFI 240
QY 241 IIAVFICFVPHFARIPYTLISQTRDVFDCIAENTLFFVKESTLMLTSLNCLDPFIYFF 300
Db 241 IIAVFICFVPHFARIPYTLISQTRDVFDCIAENTLFFVKESTLMLTSLNCLDPFIYFF 300
QY 301 LCKSFNSLSMLKCPNSATSLSDNRRKKEDGDGDPNEETPM 342
Db 301 LCKSFNSLSMLKCPNSATSLSDNRRKKEDGDGDPNEETPM 342

RESULT 13
AAE04385
ID AAE04385 standard; Protein: 315 AA.
AC AAE04385;
XX
DN 04-SEP-2001 (first entry)
XX
DE Human P2-purinegic receptor subtype, P2Y12 protein fragment.
XX
KW Human; P2-purinegic receptor; P2Y12; cardiac; vasotropic; thrombolytic;
KW cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina;
KW myocardial infarction; ischaemic attack; pre-eclampsia; bleeding disorder;
KW carotid endarterectomy; vascular graft surgery; brain disorder; migraine;
KW vascular injury; schizophrenia; eating disorder; depression; angioplasty;
KW peripheral vascular disease; platelet aggregation; restenosis; embolism;
KW thrombocytopenic purpura; stroke; perustis toxin-sensitive G protein;
KW GI; disseminated intravascular coagulation; thrombosis.
XX
OS Homo sapiens.
XX
PN WO200146454-A1.
PD 28-JUN-2001.
XX
PF 26-DEC-2000; 2000WO-US34998.
XX
PR 23-DEC-1999; 99US-0171622.
XX
PA (CORT-) COR THERAPEUTICS INC.
PI Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;
PI Holloper G;
XX
DR WPI: 2001-418082/44.
DR N-PSDB: AAD08694.
XX

```

PT Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful
 for identifying binding partners and for diagnostic applications -
 XX
 PS Example 1; Page 84-85; 108pp; English.
 CC The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed
 CC as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is
 CC the subtype of P2-purine receptor. The P2Y12 receptor is expressed
 CC selectively in the platelets and brain, and couples to a pertussis toxin-
 CC sensitive G protein (G_i). P2Y12 receptor is a G protein-coupled receptor
 CC that responds to ADP. The invention also relates to a method for
 CC identifying an agent which is useful for modulating acute myocardial
 CC infarction, unstable angina, chronic stable angina, transient ischaemic
 CC attacks, strokes, peripheral vascular disease, pre-eclampsia, deep venous
 CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic
 CC thrombocytopenic purpura or a bleeding disorder; thrombotic and
 CC restenotic complications following angioplasty, carotid endarterectomy,
 CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery,
 CC stent placements or insertion of endovascular devices and prostheses.
 CC P2Y12 receptor is useful for identifying binding partners and for
 CC diagnostic applications. P2Y12 receptor provides targets for screening
 CC synthetic small molecules and combinatorial or naturally occurring
 CC compound libraries to regulate platelet aggregation, vascular injury, or
 CC disease as well as schizophrenia, eating disorders, depression, migraine
 CC and other brain disorders. The present sequence is a fragment of human
 CC P2-purine receptor subtype, referred as P2Y12.
 CC
 XX
 SQ Sequence 315 AA;
 Query Match 91.9%; Score 1634; DB 22; Length 315;
 Best Local Similarity 100.0%; Pred. No. 3.2e-171;
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQADVNTSAPGNTSLCTRDYKIQVLFPLLYVLFVGLITNGLAMRIFFQIRSKSNFI 60
 DB 1 MQADVNTSAPGNTSLCTROKRIQVLFPLLYVLFVGLITNGLAMRIFFQIRSKSNFI 60
 QY 61 IFLKNVYISDLMLTTPFKILSDAKLGTGPLRFVQCVSVIYFTWYISISFLGLITI 120
 DB 61 IFLKNVYISDLMLTTPFKILSDAKLGTGPLRFVQCVSVIYFTWYISISFLGLITI 120
 QY 121 DRYOKTRPFTSNPKMLGAKLISVYIMAFMFLSLPNMILTNRQPKDKVKKCSFLKS 180
 DB 121 DRYOKTRPFTSNPKMLGAKLISVYIMAFMFLSLPNMILTNRQPKDKVKKCSFLKS 180
 QY 181 EFLGVMHEIYVYICQVLFMIFNLIVCYLTITKELRSYVRFGVGVPRKKVNVKFI 240
 DB 181 EFLGVMHEIYVYICQVLFMIFNLIVCYLTITKELRSYVRFGVGVPRKKVNVKFI 240
 QY 241 IIAVFICFPFHFARIPYTLSTQRDVDCFAENTLFEYKESTLMTLSLNACDPFIYFF 300
 DB 241 IIAVFICFPFHFARIPYTLSTQRDVDCFAENTLFEYKESTLMTLSLNACDPFIYFF 300
 QY 301 LCKSFRNSLISMLKC 315
 DB 301 LCKSFRNSLISMLKC 315
 RESULT 14
 AAM48354
 ID AAM48354 standard: Protein; 347 AA.
 AC AAM48354;
 XX
 XX 25-APR-2002 (first entry)
 DE Murine G protein-coupled receptor, IGPCRI7.
 XX
 XX Murine; G protein-coupled receptor; IGPCRI7; analgesic; neuroleptic;
 KW transducer; antiparkinsonian; neuroprotective; nootropic;
 KW anticonvulsant; metabolic; anorectic; anabolic; antiinflammatory;
 KW antidiarrhetic; osteopathic; antiasthmatic; antiallergic; antiarthritic;
 KW immunosuppressive; gene therapy; psychiatric disorder;

KW central nervous system disorder; movement dysfunction; schizophrenia;
 KW multiple sclerosis; Alzheimer's disease; kidney disease; obesity;
 KW gastrointestinal disorder; osteoporosis; infection;
 KW gynecological disorder; receptor.
 OS Mus musculus.
 XX
 XX W0200202599-A2.
 PN
 XX 10-JAN-2002.
 PD
 XX
 XX 02-JUL-2001; 2001WO-EP07532.
 PF
 XX 30-JUN-2000; 2000US-215759P.
 PR
 XX (INGE-) INGENIUM PHARM AG.
 PA
 XX Wattler F, Wattler S, Trommler P, Nehls MC;
 PI
 XX WPI: 2002-140080/18.
 DR
 XX N-PSDB; ABA98539.
 DR
 XX
 PT New human or mouse G protein-coupled receptor protein, IGPCRI7, useful
 PT for diagnosis, prevention, amelioration or treatment of central nervous
 PT system disorders such as Tourette's syndrome, Parkinson's disease and
 PT pain -
 PT
 XX
 XX Claim 9; Fig 6; 71pp; English.
 PS
 XX
 CC The present sequence is the protein sequence for murine G protein-coupled
 CC receptor (GPCR) protein, IGPCRI7. The coding sequence for IGPCRI7 is
 CC useful in gene therapy for prevention, amelioration or treatment of
 CC diseases characterised by aberrant expression or activity of IGPCRI7,
 CC where the disease is a psychiatric or central nervous system (CNS)
 CC disorder associated with signal processing in CNS such as learning and
 CC memory disorders, movement dysfunctions, tics, tremor, Tourette's
 CC syndrome, Parkinson's disease, Huntington's disease, dyskinesias,
 CC dystonia, pain and spasms. In addition, IGPCRI7 and its coding sequence
 CC are useful in diagnosis, prevention, amelioration or treatment of
 CC diseases associated with signal processing in CNS, schizophrenia,
 CC episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive
 CC disorder (OCD), multiple sclerosis, Alzheimer's disease/dementia,
 CC anorexia, kidney diseases such as renal failure, obesity,
 CC gastrointestinal disorders such as irritable bowel syndrome (IBS),
 CC diarrhoea, motility disorders and conditions of delayed gastric emptying,
 CC osteoporosis, infections such as bacterial, fungal, protozoal and viral
 CC infections, asthma, allergy, arthritis, sepsis and gynecological
 CC disorders.
 CC
 XX
 SQ Sequence 347 AA;
 Query Match 87.5%; Score 1555.5; DB 23; Length 347;
 Best Local Similarity 88.7%; Pred. No. 1.6e-162;
 Matches 299; Conservative 16; Mismatches 21; Indels 1; Gaps 1;
 QY 6 NLTSAPGNTSLCTRDYKIQVLFPLLYVLFVGLITNGLAMRIFFQIRSKSNFIIFLKN 65
 DB 12 NLTSPGNTSLCTRDYKIQVLFPLLYVLFVGLITNGLAMRIFFQIRSKSNFIIFLKN 71
 QY 66 TVISDMLMLTTPFKILSDAKLGTGPLRFVQCVSVIYFTWYISISFLGLITIDRYOK 125
 DB 72 TVISDMLMLTTPFKILSDAKLGTGPLRFVQCVSVIYFTWYISISFLGLITIDRYOK 131
 QY 126 TTRPFTSNPKMLGAKLISVYIMAFMFLSLPNMILTNRQPKDKVKKCSFLKSEGLV 185
 DB 132 TTRPFTSNPKMLGAKLISVYIMAFMFLSLPNMILTNRQPKDKVKKCSFLKSEGLV 191
 QY 186 WHEIVNYICQVLFMIFNLIVCYLTITKELRSYVRFGVGVPRKKVNVKFIIAV 245
 DB 192 WHEIVNYICQVLFMIFNLIVCYLTITKELRSYVRFGVGVPRKKVNVKFIIAV 251
 QY 246 FICFVPFHFARIPYTLSTQRDVDCFAENTLFEYKESTLMTLSLNACDPFIYFLCKSF 305
 DB 246 FICFVPFHFARIPYTLSTQRDVDCFAENTLFEYKESTLMTLSLNACDPFIYFLCKSF 305

Db 252 FICFVPHFARIPYTLISQTRAVFDCNAENTLFYVKESTLMLTSLNACLDPEIFYFLCKSF 311

QY 306 RNSLISMILKCPNSATSLSQDNKKKEQDGDPNETPM 342

Db 312 RNSLISMILKCPNSATSLSQDNKKKEQDGDPNETPM 347

RESULT 15

AAE04384 standard; Protein: 343 AA.

AAE04384:

AC AAE04384:

XX 04-SEP-2001 (first entry)

XX

DE Rat P2-purinerbic receptor subtype, P2Y12.

XX

XX Rat: P2-purinerbic receptor; P2Y12; cardiant; vasotropic; thrombolytic; cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina; myocardial infarction; ischaemic attack; preclampsia; bleeding disorder; carotid endarterectomy; vascular graft surgery; brain disorder; migraine; vascular injury; schizophrenia; eating disorder; depression; angioplasty; peripheral vascular disease; platelet aggregation; restenotic; embolism; thrombocytopenic purpura; stroke; pertussis toxin-sensitive G protein; GI: disseminated intravascular coagulation; thrombosis.

XX

OS Rattus norvegicus.

XX

PN W0200146454-A1.

XX

PD 28-JUN-2001.

XX

PE 26-DEC-2000; 2000WO-US34998.

XX

XX 23-DEC-1999; 99US-0171622.

XX

PA (COR-) COR THERAPEUTICS INC.

XX

PI Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ,

PI Hollopeter G;

XX

DR WPI: 2001-418082/44.

DR N-PSDB: AAD08693.

XX

PT Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful

PT for identifying binding partners and for diagnostic applications

XX

XX Claim 14: Page 81-82; 108pp; English.

XX

XX The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is the subtype of P2-purinerbic receptor. The P2Y12 receptor is expressed selectively in the platelets and brain, and couples to a pertussis toxin-sensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor that responds to ADP. The invention also relates to a method for identifying an agent which is useful for modulating acute myocardial infarction, unstable angina, chronic stable angina, transient ischaemic attacks, strokes, peripheral vascular disease, preclampsia, deep venous thrombosis, embolism, disseminated intravascular coagulation, thrombotic thrombocytopenic purpura or a bleeding disorder; thrombotic and restenotic complications following angioplasty, carotid endarterectomy, post CABG (coronary artery bypass graft) surgery, vascular graft surgery, stent placements or insertion of endovascular devices and prostheses. P2Y12 receptor is useful for identifying binding partners and for diagnostic applications. P2Y12 receptor provides targets for screening synthetic small molecules and combinatorial or naturally occurring compound libraries to regulate platelet aggregation, vascular injury, or disease as well as schizophrenia, eating disorders, depression, migraine and other brain disorders. The present sequence is rat P2-purinerbic receptor subtype, referred as P2Y12 receptor.

XX

Sequence 343 AA;

50

Query Match 86.0%; Score 1528.5; DB 22; Length 343;

Best Local Similarity 86.9%; Pred. No. 1,3e-159;

Matches 293; Conservative 17; Mismatches 22; Indels 5; Gaps 1;

QY 6 NLTSAAGNTSLCTRDYKLTQVLEPLLTVLFFVGLITNGLAMRIFFOIRKSNFIIFLKN 65

Db 12 NLTSAAGNTSLCTRDYKLTQVLEPLLTVLFFVGLITNGLAMRIFFOIRKSNFIIFLKN 71

QY 66 TVISDLMLITLFFPKILSDAKLGTGRLPTFVQVTSVIFETMVISISPLGLITDRYOK 125

Db 72 TVISDLMLITLFFPKILSDAKLGTGRLPTFVQVTSVIFETMVISISPLGLITDRYOK 131

QY 126 TTRPKTSPNPKNLGAKILSVYNAFMFLSLPNMILINRQPRDKNVKCSFLSEGLV 185

Db 132 TTRPKTSPNPKNLGAKILSVYNAFMFLSLPNMILINRQPRDKNVKCSFLSEGLV 191

QY 186 WHEIYNYICQVIFWIFNLIVICVFLITKELRSYVTRGVKVRKKNVNFIIIVF 245

Db 192 WHEIYNYICQVIFWIFNLIVICVFLITKELRSYVTRGVKVRKKNVNFIIIVF 251

QY 246 FICFVPHFARIPYTLISQTRAVFDCNAENTLFYVKESTLMLTSLNACLDPEIFYFLCKSF 305

Db 252 FICFVPHFARIPYTLISQTRAVFDCNAENTLFYVKESTLMLTSLNACLDPEIFYFLCKSF 311

QY 306 RNSLISMILKCPNSATSLSQDNKKKEQDGDPNETPM 342

Db 312 RNSLISMILKCPNSATSLSQDNKKKEQDGDPNETPM 343

Search completed: December 6, 2002, 10:06:09

Job time : 40 secs


```
Patent No. 6162899
GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: HALSEY, WENDY
APPLICANT: MUIR, ALISON
APPLICANT: CHAMBERS, JON
APPLICANT: SZEKERES, PHILIP
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS
AND ANTAGONISTS OF THE HNEA81 RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestla
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,456
FILING DATE: 28-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,975
FILING DATE: 23-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestla, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70318-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-221-456-2

Query Match          46.3%; Score 823; DB 4; Length 333;
Best Local Similarity 48.7%; Pred. No. 5,9e-63;
Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;
```

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RESULT 3
US-09-558-740-2
Sequence 2, Application US/09558740
Patent No. 6358695
GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: HALSEY, WENDY
APPLICANT: MUIR, ALISON
APPLICANT: CHAMBERS, JON
APPLICANT: SZEKERES, PHILIP
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
ANTAGONISTS OF THE HNEA81 RECEPTOR
FILE REFERENCE: GH-70318-2
CURRENT APPLICATION NUMBER: US/09/558,740
CURRENT FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 08/956,975
PRIOR FILING DATE: 1997-10-23
PRIOR APPLICATION NUMBER: 09/221,456
PRIOR FILING DATE: 1998-12-28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 333
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-558-740-2

Query Match          46.3%; Score 823; DB 4; Length 333;
Best Local Similarity 48.7%; Pred. No. 5,9e-63;
Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;
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; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,871
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0237 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: MBLR3DT01
; CLONE: 568987
; US-08-812-871-1

Query Match 44.8%; Score 797; DB 2; Length 333;
Best Local Similarity 47.8%; Pred. No. 9.8e-61;
Matches 151; Conservative 57; Mismatches 106; Indels 2; Gaps 1;

QY 17 CTRDYKIQVLEPLLTYLVFVGLITNGILNARIFQIRSKSNFIILKNTVISDLMILT 76
DB 15 CPRDRRIQVLPALYVFLGILNLTALVFAHVPSSFFIYKNTLVADLIMLTLM 74
QY 77 FPEKLSAKLGTPGLRTFVQVTSVIFYFTMYISISFLGLITIDRYOKTTPEFKTSNPK 136
DB 75 LPEKLSLSHAPMQLRANFVCFSSVIEFTYVGVILGLIAPDRFKLIIPLNRIELK 134
QY 137 NLGAKITSVVAEMFPLSLPNMILITNROPDRKNVKKCSFLKSEGLVWHEIVNYICOV 196
DB 135 KPVFKATYSIFLWFLFISLIPMILSNKEATPSSVKKCASLKGFLGLKMHOMVNNICOF 194
QY 197 IFWINEFLIVCYTLITRELYRSYVRTRGVGKVPKKNVKKVFIIVAFICVPEHFAR 256
DB 195 IFWVLIILMLVYVYIAKVVOSYRKSCKDRKNKKEGKVVVVVPEVFCFAPFHAR 254
QY 257 IPYTSISQRDVDCIAENTLIFYKESTIMLTLNLACDPEFIYFLCKSRNLSIMLKP 316
DB 255 VPTYSQSNKNNKDKLQNLQFLAKETTLATATNLCMDPLISFLCKRTEKTEPCMQ--G 312
QY 317 NSATSLSDNNRKEOD 332
DB 313 RKTASSQENHSSQTD 328

```

RESULT 5
US-08-467-948A-29
Sequence 29, Application US/08467948A
Patent No. 5998164
GENERAL INFORMATION:

APPLICANT: LI, YI
APPLICANT: CAO, LI, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.

```

; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
; TITLE OF INVENTION: Coupled Receptor GPR2
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,948A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04079
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STEEFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-467-948A-29

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Query Match 43.4%; Score 772; DB 2; Length 325;
Best Local Similarity 47.5%; Pred. No. 1.3e-58;
Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

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QY 6 NLTSAPAGNTSLCTRDYKIQVLEPLLTYLVFVGLITNGILNARIFQIRSKSNFIILKLN 65
DB 2 NSTSQPPDESQSNLITQIIPVLYCWFIAIGLLNGVSGWIFVYVSSKSFIIYKLN 61
QY 66 TVISDLMILTRPEKLSAKLGTPGLRTFVQVTSVIFYFTMYISISFLGLITIDRYOK 125
DB 62 IVIADFVMSLTPPEKILGDSGLGPMQNLNFVCRSAVLFTYVMYVSIYFFGLISFDRYK 121
QY 126 TTRPRTSNPKLNLAKITSVVAEMFPLSLPNMILITNROPDRKNVKKCSFLKSEFLV 185
DB 122 IYKPLMTSFTQSVYSKLSLIVMMILMLAVNIIITNQSVREYQICIELKSELGK 181
QY 186 WHEIYNYICOVFWINEFLIVCYTLITRELYRSYVRTRGVGKVPKKNVAVFIIVAF 245
DB 182 WHKASNYIFVALFWIYVFLIIVFYTAIFKKIFKSHKSSRNSTSVKKSRRNIFSIYFV 241
QY 246 FTCEVPEHFARIPYTSISQRDVDCIAENTLIFYKESTIMLTLNLACDPEFIYFLCKSE 305
DB 242 FVCFVPHYHARIPYTSISQREAHYSCOSKEILRYMKREFTLLSAAVNCIDPIYFELCOPE 301
QY 306 RNSLSMLKCPNSA 319
DB 302 RELCKKLIHPLKA 315

```

RESULT 6
US-08-467-947A-29
Sequence 29, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:

APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULL, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STERFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SRO ID NO: 29
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-947A-29

Query Match 43.4%; Score 772; DB 3; Length 325;
Best Local Similarity 47.5%; Pred. No. 1.3e-58;
Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

DB 6 NLTSAPGNTSLCTRDYKITQVLFPLLYTVLEFVGLITNGLAMRIFFQIRSKSNFIIFLKN 65
DB 2 NSTSTOPDESCSONLITQOIIPLVLCWFIAGILNGVSGWIFVFPSSKSPFIYLYKN 61
DB 66 TVISDLMILFFPKRIISDAKIGTGPLRTFVCOYTSVFEYTWYISISFLGLITIDRYOK 125
DB 62 IVIADFVMSLTFPPKRIISDAKIGTGPLRTFVCOYTSVFEYTWYISISFLGLITIDRYOK 121
DB 126 TTRPFTKSNPKNLGAKILSVINAFMFLSLPMNLTNRQPRDKNVKCSFLKSEGLV 185
DB 122 IVKPLMTSFIOSVSKLSIYVMMLLAVPNIIITNOSVREVTQIKTELKSELGRK 181
DB 186 WHEIVNTICQVIFINFLIVYCYTLITKELYSVRTRGVGVPRKKVNVKVEIIIAVF 245
DB 182 WHKASNTYFVAIFWIVFLLIVFYATITKKIKFKSHLSSRSNSTSVKKSNNIFSIVFV 241
DB 246 FICVPPHFARIPYTLSTQTRVDFCTAENTLFYVKESTLMTSLTNACIDPIYFFLCKSF 305
DB 242 FVCEVPFHAIAPITKSTGTEHAYSCQSLIRYKMEFTLLISANVCIDPIYFFLCKSF 301
DB 306 RNSLSMLKCPNSA 319
DB 302 REICKKLIHPLKA 315

RESULT 7
US-08-988-876-8
Sequence 8, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SRO ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 338 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 285995
US-08-988-876-8

Query Match 43.4%; Score 772; DB 3; Length 338;
Best Local Similarity 47.5%; Pred. No. 1.4e-58;
Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

DB 6 NLTSAPGNTSLCTRDYKITQVLFPLLYTVLEFVGLITNGLAMRIFFQIRSKSNFIIFLKN 65
DB 3 NSTSTOPDESCSONLITQOIIPLVLCWFIAGILNGVSGWIFVFPSSKSPFIYLYKN 62
DB 66 TVISDLMILFFPKRIISDAKIGTGPLRTFVCOYTSVFEYTWYISISFLGLITIDRYOK 125
DB 63 IVIADFVMSLTFPPKRIISDAKIGTGPLRTFVCOYTSVFEYTWYISISFLGLITIDRYOK 122
DB 126 TTRPFTKSNPKNLGAKILSVINAFMFLSLPMNLTNRQPRDKNVKCSFLKSEGLV 185
DB 123 IVKPLMTSFIOSVSKLSIYVMMLLAVPNIIITNOSVREVTQIKTELKSELGRK 182
DB 186 WHEIVNTICQVIFINFLIVYCYTLITKELYSVRTRGVGVPRKKVNVKVEIIIAVF 245
DB 183 WHKASNTYFVAIFWIVFLLIVFYATITKKIKFKSHLSSRSNSTSVKKSNNIFSIVFV 242
DB 246 FICVPPHFARIPYTLSTQTRVDFCTAENTLFYVKESTLMTSLTNACIDPIYFFLCKSF 305

Db 243 FVCCVPRIHARIPPTKQTEAHNSCQSKELIRYKETTLLLSAANCWLDPIIIFFLCQPF 302D

QY 306 RNSLSMLKCPNSA 319

Db 303 REILCKKLIHPLKA 316

RESULT 8

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US-09-303-524A-2
: Sequence 2, Application US/09303524A
: Patent No. 6238873
: GENERAL INFORMATION:
: APPLICANT:
: APPLICANT: CHAMBERS, JONATHAN K.
: APPLICANT: STEWART, BRIAN R.
: APPLICANT: AMES, ROBERT S.
: APPLICANT: SARAU, HENRY M.
: APPLICANT: FOLEY, JIM
: APPLICANT: ARNOLD, ANNE ROMANIC
: TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
: TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN THE HUMAN KIAA0001
: TITLE OF INVENTION: RECEPTOR AND LIGANDS THEREOF
: FILE REFERENCE: GP50007
: CURRENT APPLICATION NUMBER: US/09/303,524A
: PRIORITY FILING DATE: 1999-04-30
: PRIORITY FILING DATE: 1998-05-01
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 338
: TYPE: PR1
: ORGANISM: Homo sapiens
: US-09-303-524A-2

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Query Match	43.4%	Score 772;	DB 4;	Length 338;
Best Local Similarity	47.5%	Pred. No. 1.4e-58;		
Matches 149; Conservative	60;	Mismatches 105;	Indels 0;	Gaps 0;

[illegible]

RESULT 9

US-08-988-876-3
Sequence 3, Application US/089888876
Patent No. 6065596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry

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Best Local Similarity	43.78	Pred. No. 1.1e-50		
Matches 132	Conservative 64	Mismatches 99	Indels 7	Gaps 4

[illegible]

RESULT 10

US-08-467-948A-6
; Sequence 6, Application US/08467948A

Patent No 5998164
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULLT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-948A-6

Db 243 ICFVPHHVOIPWTIAEL-GMPSSNHQAIINDAHQVITICLSTNCVLDPVITCYFLTKKR 301
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Db 302 KHLSEKLNIMRSSQKCSRVTDTGTENAIPIINHTPV 337

Search completed: December 6, 2002, 10:08:19
Job time : 16 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2002, 10:06:15 ; Search time 119 Seconds
(without alignments)
46.680 Million cell updates/sec

Title: US-09-835-922-2
Perfect score: 1778
Sequence: 1 MQAVNLTSAFGNTSLCTRD.....SQDNRRKEDGGDPNEETPM 342

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues
Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1778	100.0	342	9	US-09-964-008-1
2	1778	100.0	342	10	US-09-835-922-2
3	1778	100.0	342	10	US-09-827-937A-2
4	1778	100.0	342	10	US-09-780-576-2
5	1748	98.3	342	9	US-09-964-008-3
6	823	46.3	333	10	US-09-769-159-2
7	797	44.8	333	10	US-09-848-889-1
8	772	43.4	338	10	US-09-919-497-7
9	741.5	39.1	338	10	US-09-826-508-20
10	694.5	38.2	358	9	US-09-826-508-10
11	679.5	38.2	358	9	US-09-919-172-22
12	679.5	38.2	319	12	US-10-025-335-1
13	488	27.4	327	12	US-10-084-206-3
14	385	21.7	327	12	US-10-084-206-3
15	376	21.1	348	10	US-09-827-937A-17
16	374.5	21.1	381	10	US-09-997-522-2
17	347.5	19.5	330	10	US-09-826-791-2
18	347.5	19.5	346	9	US-09-828-478-2
19	347.5	19.5	346	10	US-09-826-791-6

20	347.5	19.5	346	10	US-09-866-230-7	Sequence 7, Appl1
21	347.5	19.5	346	10	US-09-866-230-9	Sequence 9, Appl1
22	334	18.8	367	9	US-09-828-478-6	Sequence 6, Appl1
23	329.5	18.5	299	9	US-09-860-670-81	Sequence 81, Appl1
24	329.5	18.5	299	10	US-09-764-853-521	Sequence 521, App
25	329.5	18.5	339	9	US-09-828-478-4	Sequence 4, Appl1
26	329.5	18.5	339	10	US-09-848-889-12	Sequence 12, Appl1
27	329.5	18.5	339	10	US-09-788-133-2	Sequence 2, Appl1
28	321	18.1	359	9	US-09-867-569-9	Sequence 9, Appl1
29	317.5	17.9	398	10	US-09-823-114-16	Sequence 16, Appl1
30	317.5	17.9	398	10	US-09-966-871-1	Sequence 1, Appl1
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32	315	17.7	405	10	US-09-966-871-84	Sequence 84, Appl1
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34	314.5	17.7	398	10	US-09-966-871-81	Sequence 79, Appl1
35	314.5	17.7	398	12	US-10-039-645-79	Sequence 79, Appl1
36	313	17.6	382	10	US-09-993-844-4	Sequence 4, Appl1
37	313	17.6	415	10	US-09-823-114-20	Sequence 20, Appl1
38	312	17.5	359	10	US-09-966-871-81	Sequence 81, Appl1
39	312	17.5	359	12	US-10-039-645-81	Sequence 81, Appl1
40	309.5	17.4	380	10	US-09-149-045-2	Sequence 2, Appl1
41	309	17.4	400	10	US-09-966-871-85	Sequence 85, Appl1
42	309	17.4	400	12	US-10-039-645-85	Sequence 85, Appl1
43	306	17.2	400	10	US-09-966-871-78	Sequence 78, Appl1
44	306	17.2	400	12	US-10-039-645-78	Sequence 78, Appl1
45	305	17.2	400	10	US-09-966-871-86	Sequence 86, Appl1

ALIGNMENTS

RESULT 1

US-09-964-008-1

Sequence 1, Application US/09964008

Patent No. US20020156246A1

GENERAL INFORMATION:

APPLICANT: Glucksmann, Maria A.

APPLICANT: Gu, Wei

TITLE OF INVENTION: 15625 Receptor, A No. US20020156246A1el G-Protein Coupled Rece

FILE REFERENCE: 5800-13, 035800-171548

CURRENT APPLICATION NUMBER: US/09/964, 008

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 09/187,134

PRIOR FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 342

TYPE: PRT

ORGANISM: Homo sapiens

US-09-964-008-1

Query Match	100.0%	Score 1778:	DB 9:	Length 342:
Best Local Similarity	100.0%	Pred. No. 5.8e-151;		
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Gaps 0;				
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DB	61	IFLKNTVISDLMLTFPPKILSDAKLGTPLRTEVCQVTVIFFTWYISISFLGLITI	120	
QY	121	DVYQTTREFTSNRKNLIGAKILSVVMAEFLSLPMIITNQPORKNVKCSFLKS	180	
DB	121	DVYQTTREFTSNRKNLIGAKILSVVMAEFLSLPMIITNQPORKNVKCSFLKS	180	
QY	181	ERGLVWHEIVNTICQVIFINFLIVCYTLITKELRSYVTRGVGKPRKKNVYKVI	240	
DB	181	ERGLVWHEIVNTICQVIFINFLIVCYTLITKELRSYVTRGVGKPRKKNVYKVI	240	
QY	241	ITAVFICFPVPHARIPYTLISQTRVDVDCATENTLFYKESTLMTLSINACLDPIFYFF	300	

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Db 241 IIAVFICFVPHFARIPYLSQTRDVDCDAENTLIFYVESTLMLSLNACLDPEIFYFF 300
QY 301 LCKSFNSLSMLKCPNSATSLSDNRRKKEQDGDGDPNEETPM 342
Db 301 LCKSFNSLSMLKCPNSATSLSDNRRKKEQDGDGDPNEETPM 342
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RESULT 2

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US-09-835-922-2
; Sequence 2, Application US/09835922
; Patent No. US20010046497A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Fang L.
; APPLICANT: Luo, Lin
; APPLICANT: Gustafson, Eric
; APPLICANT: Liu, Yan-Hui
; APPLICANT: Chen, Guodong
; TITLE OF INVENTION: G-Protein Coupled Receptor and Methods
; FILE REFERENCE: CN01167K
; CURRENT APPLICATION NUMBER: US/09/835,922
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 60/199,041
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 342
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-835-922-2
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Query Match 100.0%; Score 1778; DB 10; Length 342;
Best Local Similarity 100.0%; Pred. No. 5,8e-151;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 181 EFGLVMEIYVYICQVIFWINEFLIVICYTLITKELYSYVTRRGVGRKRVKRVKVEFI 240
QY 241 IIAVFICFVPHFARIPYLSQTRDVDCDAENTLIFYVESTLMLSLNACLDPEIFYFF 300
Db 241 IIAVFICFVPHFARIPYLSQTRDVDCDAENTLIFYVESTLMLSLNACLDPEIFYFF 300
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RESULT 3

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US-09-827-937A-2
; Sequence 2, Application US/09827937A
; Patent No. US20020052043A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruden, Steven M.
; TITLE OF INVENTION: Human G-Protein Coupled Receptors
; FILE REFERENCE: 1488,1220003
; CURRENT APPLICATION NUMBER: US/09/827,937A
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 08/852,824
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; PRIOR FILING DATE: 1997-05-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-937A-2
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Best Local Similarity 100.0%; Pred. No. 5,8e-151;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 IFKNTVYISDLMLITPEPKILSDAKLGCTGPLRTFVCQVSVIFYFTMYISISFLGLITI 120
QY 121 DRYOKTTRPEKTSNPKMLGAKILSVYIMAFMFLSLPNNMILTRNRPDRKNVKKCSFLKS 180
Db 121 DRYOKTTRPEKTSNPKMLGAKILSVYIMAFMFLSLPNNMILTRNRPDRKNVKKCSFLKS 180
QY 181 EFGLVMEIYVYICQVIFWINEFLIVICYTLITKELYSYVTRRGVGRKRVKRVKVEFI 240
Db 181 EFGLVMEIYVYICQVIFWINEFLIVICYTLITKELYSYVTRRGVGRKRVKRVKVEFI 240
QY 241 IIAVFICFVPHFARIPYLSQTRDVDCDAENTLIFYVESTLMLSLNACLDPEIFYFF 300
Db 241 IIAVFICFVPHFARIPYLSQTRDVDCDAENTLIFYVESTLMLSLNACLDPEIFYFF 300
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Db 301 LCKSFNSLSMLKCPNSATSLSDNRRKKEQDGDGDPNEETPM 342
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RESULT 4

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US-09-780-576-2
; Sequence 2, Application US/09780576
; Patent No. US20020072072A1
; GENERAL INFORMATION:
; APPLICANT: Clivelli, Olivier
; APPLICANT: Wang, Zhwei
; APPLICANT: Reinscheid, Rainer
; TITLE OF INVENTION: Adp-Glucose Receptor
; FILE REFERENCE: P-UC 4530
; CURRENT APPLICATION NUMBER: US/09/780,576
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/234,025
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-576-2
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Best Local Similarity 100.0%; Pred. No. 5,8e-151;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 181 EFGIWMHEIVNYICQVITWINEFLIYVCYTLITKELYSYVTRGVGVPRKKVAVKVI 240
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Db 241 IIAVEFICFVPHFARIPYTLISQTRDVFDCIAENTLFFYVKESTLMLTSLNACLDPEIYFF 300
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RESULT 5
US-09-964-008-3
; Sequence 3, Application US/09964008
; Patent No. US20020156246A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 15625 Receptor. A No. US20020156246A1e1 G-Protein Coupled Receptor
; FILE REFERENCE: 5800-13, 035800-171548
; CURRENT APPLICATION NUMBER: US/09/964,008
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/187,134
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Macaca sp.
US-09-964-008-3

Query Match 98.3%; Score 1748; DB 9; Length 342;
Best Local Similarity 98.0%; Pred. No. 2,7e-148;
Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Db 1 MOAANDLTSAGNLSICRDYKITQVLEPLLITYVLEFGLITNSLAMRIFQIRKSNFI 60
QY 61 IFLKNTVSDLMILITFEFFKILSDAKLGTGPLRTFVCQVTSVIEFTWYISISFGLITI 120
Db 61 IFLKNTVSDLMILITFEFFKILSDAKLGTGPLRTFVCQVTSVIEFTWYISISFGLITI 120
QY 121 DRYQKTTPEPTSPNKNLGAKILSVIWMAFMFLSLPNNMLITNRQPDKNVKKCSFLKS 180
Db 121 DRYQKTTPEPTSPNKNLGAKILSVIWMAFMFLSLPNNMLITNRQPDKNVKKCSFLKS 180
QY 181 EFGIWMHEIVNYICQVITWINEFLIYVCYTLITKELYSYVTRGVGVPRKKVAVKVI 240
Db 181 EFGIWMHEIVNYICQVITWINEFLIYVCYTLITKELYSYVTRGVGVPRKKVAVKVI 240
QY 241 IIAVEFICFVPHFARIPYTLISQTRDVFDCIAENTLFFYVKESTLMLTSLNACLDPEIYFF 300
Db 241 IIAVEFICFVPHFARIPYTLISQTRDVFDCIAENTLFFYVKESTLMLTSLNACLDPEIYFF 300
QY 301 LCKSFRNSLIISMLKCPNSATSLSDNRRKKEDGGDPNNEETPM 342
Db 301 LCKSFRNSLIISMLKCPNSATSLSDNRRKKEDGGDPNNEETPM 342

RESULT 6
US-09-769-159-2
; Sequence 2, Application US/09769159
; Patent No. US20010021509A1
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH M.

```

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APPLICANT: HALSEY, WENDY S.
APPLICANT: CHAMBERS, JON
APPLICANT: MUIR, ALISON
APPLICANT: SEZERES, PHILIP
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS OF THE HNEA81 RECEPTOR
FILE REFERENCE: GH-70318-D3
CURRENT APPLICATION NUMBER: US/09/769,159
CURRENT FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 08/956,975
PRIOR FILING DATE: 1997-10-23
PRIOR APPLICATION NUMBER: 09/221,456
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: 09/558,740
PRIOR FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 2
LENGTH: 333
TYPE: PRN
ORGANISM: HOMO SAPIENS
US-09-769-159-2

Query Match 46.3%, Score 823; DB 10; Length 333;
Best Local Similarity 48.7%, Pred. No. 4,3e-66;
Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1.

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DB 15 CPRDRIQVOLFPAIYTVFVFLTGILNTLALMFVHIPSSSTFIYLNKTLVADLMTIM 74
QY 77 FPKILSDAKIGTGQPLRTFCQVTSVIEFTWYISISIFGLITIDRYOKTTPFPYTSNPK 136
DB 75 LPEKILSDSHLAPQGLRAFCRFSVSIVIEFTWYVGIYVLGLIAPRFLKILINPLNIFLK 134
QY 137 NLGAKILSVIYAFMFLSLPNMLTLNRQPRDKVAKKCSFLKSEFGLWHEIYVNICOV 196
DB 135 KPVAKIVSIFIEWFLFISLPNTLLSKKATPSSVKKACSLGKGLKWHQMVNNICOF 194
QY 197 IFWIFELIIVCYTLITKEILRSYVRTGCVGKVPKKRVNVKVEIILIAVEIFCFVPHFAR 256
DB 195 IFWIFELIIVFYVYIAKVVDYSKSKSKDKRKNKKLEGGKFFVYVAVFVCFAPHPHAR 254
QY 257 IPLYLSQTRDVFDECTAENTLFLYVKESTIWLWLSLNACLDPEIYFIFLCKSEFNSLISMLKCP 316
DB 255 VPYTSQTNKTKDCHLQNLQFLAKETTFIATNTICMPLIYIFLCKKTEKLPQMG--G 312
QY 317 NSATSLSDNKRKKED 332
DB 313 RKTTSQENHSSQTD 328

RESULT 7
US-09-848-889-1
Sequence 1, Application US/09848889
Patent No. US2002025555A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Cheng, Muzong
TITLE OF INVENTION: GPCR DIAGNOSTIC FOR BRAIN CANCER
FILE REFERENCE: PC-0042 CIP
CURRENT APPLICATION NUMBER: US/09/848,889
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PERL Program
SEQ ID NO: 1
LENGTH: 333
TYPE: PRN
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incycle ID NO. US20020025555A1 568987CD1

```


ORGANISM: HOMO SAPIENS
US-09-826-508-10

US-09-826-508-10

Query Match	39.1%;	Score 694.5;	DB 10;	Length 358;
Best Local Similarity	-42.2%;	Pred. No. 1.2e-54;		
Matches 139;	Conservative 68;	Mismatches 113;	Indels 9;	Gaps 5;

Qy	6	NTLSAP--NTSLSTRDVKITQVLEPRLLYVLVFEFGTLTTLAKIRIPOIKSSEITFLK	64
Db	25	NRSGPGKNKNTL---NHPEPTIVLPVYLXILIFVASILINOLAWIFPHINKRSFITYLK	81
Qy	65	NTYISDLMLITPEPKLTLSDAKLSTGCLRTFVCQVTSVIFETWYISISFLGLTIDRYO	124
Db	82	NIYVADLIMLTPEPFRIVHADGEGPWYEFKELIKRYTSVLEFAMWYTSIVELGLTIDRYL	143
Qy	125	KTRPEPKTSMPKNTLGAKILISYVIAWAFELSL--PNMLITRORPDRKKVCKSFLKSBEGL	164
Db	142	KVYKPEFDSKMYSTTFPKVLISVCWYIMAYLSPILNITLTGGPPEEDINHCOSKLSPLGV	201
Qy	185	VMEIIVNYICQVLPWINEFLVIVCYTLITKELYSYVTRGVGKVPKR--KVNVKVFIIIA	243
Db	202	KMHIAVYVWSCLEFVAALVTLICGYIISATSYIHKS--SRQFISQSSRRKHNOISIRVVA	259
Qy	244	VFFICFEPFHEARIPVYLSQTRDVFQDCLATLFFYKESYLTMTLSLACIDPLFYFLK	303
Db	260	VFFICFELPYHLCRIPFYSFHLDRILDESAOKILYCKEITLFLFSACVAVCLDPIYFFMCR	319
Qy	304	SFRNSLI--SMLKCPNSATSLSDNNRKE	330
Db	320	SFSRRLPEKKSNIIRTRSISITLSQSVRSE	348

RESULT 11
US-09-974-298-86

Sequence 86, Application US/09974298
Patent No. US20020156263A1
GENERAL INFORMATION:
APPLICANT: Chen, Huel-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 86
LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20020156263A1 1650519CDD1
US-09-974-298-86

Query Match Similarity	38.2%	Score 679.5	DB 9	Length 358
Best Local Similarity	43.7%	Pred. No. 2.6e-53		
Matches 132: Conservative	64	Mismatches 99	Indels 7	Gaps 4

[illegible]

Db 202 KWHYAVTVNSCLFVAVLVILIGCYIAISRYIHS--SRQFISQSSRKRRKHNSIRVVA 259

QY 244 VEFICFVPHFARIRYITLSQIRDVFDCTAENTFFYVKESTLWLSLNACLDPFIYFFLCK 3033

Db 260 VYFICFLPHLCRMSTFSSHDRLLDLSAQIKLYCKETLFLSACNVCLDPFIYFFMCR 3195

QY	304	SF	305
Db	320	SF	321

RESULT 12
US-09-919-172-22

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Sequence 22, Application US/09919172
Patent No. US20020119463A1
GENERAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ. ID NOS: 102
SOFTWARE: PERL Program
SEQ. ID NO 22
LENGTH: 358
TYPE: PR1
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020119463A1 1650519CD1
US-09-919-172-22

```

Query Match	38.2%	Score 679.5;	DB 10;	Length 358;
Best Local Similarity	43.7%	Pred. No. 2.6e-53;		
Matches 132; Conservative	64;	Mismatches 99;	Indels 7;	Gaps 4

[illegible]

```

CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/025,335
FILING DATE: 18-Dec-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791,974
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0198 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: 346874
US-10-025-335-1
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Query Match      27.4%, Score 488, DB 12, Length 319;
Best Local Similarity 34.5%, Pred. No. 2,4e-36;
Matches 112; Conservative 62; Mismatches 125; Indels 26; Gaps 9;

QY 13 NTSLSCTROYKKTQVLFPLLYIVLFFVGILTNGLARIPFOIKSKSNFIIFLKNTYISDL 71
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 NSSFCPCPYAKDIEPFTTFEYLVLFGIIGSCFAWAFIQKNTNHRCSYIYLINLTAE 61

QY 72 LMILTFPKRILSDANKLGTP--LRTFVCQVTVSIFEFTWYISISEFLGITTDIRYOCTRP 129
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 LITLALPVKIYVD-LGVAAPMKLIKPHQGVATCLIIYNKYLIIFLAFSIDRCQLTHS 119

QY 130 FKTSPKNULGAKLISVYIAMFELSLDPNMLITNRQPRDKAVKKCSFKSEGLWMHEI 189
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 120 CKIYRIQEPGRKAMISTVVMVLMVLINVPNMMPITKDIREKSNVCCMEFKKEFGRMHLL 179

QY 190 VNYIQGVFWFMINE-LTIIVACYTLIRKEIYSRVPTRGYGKVR-KKVNVKVFIIIAVEPI 247
   |||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 180 TNEICVALF-LNFSAILILISNCIVLRQLRN-----KDNENYNNVKALINILLVTGGTII 234

QY 248 CFVPEHFARIPTYLSQTRDVEDCTAENTLFYKESTLMTLSLNACLDPEIFYFLCKSFEN 307
   |||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 235 CFVPHYAIRIPTYSQTETVITDCSPRISLFRKAETLLLAASNLCDEPDILYYHLKAFRS 294

QY 308 SLI-----SMLKCNESA 319
   : | | | | |
Db 295 KVTETFPASPKETKAKOEKLRCENNA 319

RESULT 14
US-10-084-206-3
Sequence 3, Application US/10084206
Patent No. US20020106741A1
GENERAL INFORMATION:
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APPENDIX 11 et al.					
TITLE OF INVENTION: G-Protein Receptor HTNAD29					
FILE REFERENCE: PFI91DICI					
CURRENT APPLICATION NUMBER: US/10/084,206					
CURRENT FILING DATE: 2002-02-28					
PRIOR APPLICATION NUMBER: US95/07288					
PRIOR FILING DATE: 1995-06-06					
PRIOR APPLICATION NUMBER: 08/468,534					
PRIOR FILING DATE: 1995-06-06					
PRIOR APPLICATION NUMBER: 09/399,095					
PRIOR FILING DATE: 1999-09-20					
NUMBER OF SEQ ID NOS: 9					
SOFTWARE: PatentIn Version 3.1					
SEQ ID NO 3					
LENGTH: 327					
TYPE: PRT					
ORGANISM: Homo sapiens					
US-10-084-206-3					
Query Match	21.7%	Score 385;	DB 12;	Length 327;	
Best Local Similarity	32.6%	Pred. No. 3,6e-27;			
Matches 104; Conservative 57; Mismatches 134; Indels 24; Gaps 9					
QY 20 DKYITQVLPFLIYLVLFVVGGLITNGLAMRIFQIR--SKSNFI-IPKNTVISDLMLIT 76					
Db 6 DSEFRTYLPFLIYLVLIIFVLGVIANGVYLVWVFARLPCKKFNFKIKIFMVNLTMADMLFIT 65					
QY 77 PPFKLSADAKGTGPRFVFCOVTVSVIVFETMYISISFLGTLITDRYOKTTPRFTSNPK 136					
Db 66 LPLMIVIQNGQNMWILPRFLCNVAGCLFFINTYCSVALGLVITYNFQAVTPRIKTAQN 125					
QY 137 NLGAKILSVIV----AFMFLSLPMNMLTNRPRDK--NVKCSFLKSEFGLWME 188					
Db 126 TRRGISLSILVIWAVIAGAAAYFILLDS---TNTVPDASGSGNTVRC-PEHYEKGSVPVL 181					
QY 189 IVNYICQVIFEMINFLIVYCYTLITKELKRSYVRRRGVGRKKVYVNVKVFIIINAVFLIC 248					
Db 182 ITHIFVSEFLVFLIILFCMLVILRTLMOPVQOORNAEYVGRALMM-VCTVLAVFIIC 240					
QY 249 FVPPHFARIPTVLSQTRDVFDCTAENTLFYVKESTLMTLSLNACADPFIYFLCKSFRN- 307					
Db 241 FVPHVVGDLPTWLAEL-GFQDSKPHQALINDAQVTLCLISTGVLDPIYICPLTKKFRKH 299					
QY 308 -----SLISMKCPNSAT 320					
Db 300 LTERKYSMRSSRKCSRAT 318					
RESULT 15					
US-09-827-937A-17					
Sequence 17, Application US/09827937A					
Patent No. US20020052043A1					
GENERAL INFORMATION:					
APPLICANT: Li, Yi					
APPLICANT: Ruben, Steven M.					
TITLE OF INVENTION: Human G-Protein Coupled Receptors					
FILE REFERENCE: 1488.1220003					
CURRENT APPLICATION NUMBER: US/09/827,937A					
CURRENT FILING DATE: 2001-04-09					
PRIOR APPLICATION NUMBER: 08/852,824					
PRIOR FILING DATE: 1997-05-07					
NUMBER OF SEQ ID NOS: 18					
SOFTWARE: PatentIn Ver. 2.0					
SEQ ID NO 17					
LENGTH: 348					
TYPE: PRT					
ORGANISM: Homo sapiens					
US-09-827-937A-17					
Query Match	21.1%	Score 376;	DB 10;	Length 348;	
Best Local Similarity	26.1%	Pred. No. 2.4e-26;			
Matches 94; Conservative 83; Mismatches 153; Indels 30; Gaps 11					

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 6, 2002, 10:04:11; Search time 33 Seconds

(without alignments)
429.846 Million cell updates/sec

Title: US-09-835-922-2

perfect score: 1778

Sequence: 1 MQAVNDLITSAFGNTSLCTRD.....SQDNRRKKGQDGDPNEETPM 342

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1778	100.0	342	1 P2YC_HUMAN	Q9H244 homo sapien
2	1748	98.3	342	1 P2YC_MACPA	Q95Kc3 macaca fasc
3	1555.5	87.5	347	1 P2YC_MOUSE	Q9cpv9 mus musculu
4	1528.5	86.0	343	1 P2YC_RAT	Q9epx4 rattus norv
5	772	43.4	338	1 P2YX_HUMAN	Q15391 homo sapien
6	741.5	41.7	338	1 P2YX_MOUSE	Q9esg6 mus musculu
7	694	39.0	305	1 P2YX_RAT	Q35881 rattus norv
8	488	27.4	319	1 H963_HUMAN	Q14626 homo sapien
9	411.5	23.1	375	1 GP34_MOUSE	Q941k6 mus musculu
10	409.5	23.0	381	1 GP34_HUMAN	Q9upc5 homo sapien
11	394	22.2	342	1 PAFR_HUMAN	P25105 homo sapien
12	392.5	22.1	342	1 PAFR_CAVPO	P21556 cavia porce
13	379.5	21.3	361	1 EB12_HUMAN	P32249 homo sapien
14	367	20.6	345	1 CLT2_PIG	Q95n03 sus scrofa
15	366	20.6	341	1 PAFR_MOUSE	Q62035 mus musculu
16	362	20.4	341	1 PAFR_RAT	P46002 rattus norv
17	357.5	20.1	308	1 P2Y5_CHICK	P32250 gallus gall
18	347.5	19.5	346	1 CLT2_HUMAN	Q91875 homo sapien
19	347.5	19.5	537	1 P2Y8_XENLA	P79928 xenopus lae
20	344	19.3	309	1 CLT2_MOUSE	Q970a1 mus musculu
21	339.5	19.1	309	1 CLT2_RAT	Q924t9 rattus norv
22	339	19.1	359	1 AG2R_BOVIN	P25104 bos taurus
23	338	19.0	344	1 P2Y5_HUMAN	P43657 homo sapien
24	334	18.8	359	1 AG2R_SHEEP	Q75990 ovis aries
25	334	18.8	367	1 GP17_HUMAN	Q13304 homo sapien
26	329	18.5	359	1 AG2S_HUMAN	Q13725 homo sapien
27	328	18.4	340	1 CLT1_PIG	Q95n02 sus scrofa
28	327	18.4	359	1 AG2R_PIG	P35555 sus scrofa
29	326	18.3	359	1 AG2R_CANFA	P43240 canis fam11
30	325.5	18.3	399	1 PAR2_MOUSE	P55086 mus musculu
31	325	18.3	359	1 AG2R_RABIT	P34976 oryctolagus
32	321	18.1	359	1 AG2R_HUMAN	P30556 homo sapien
33	320	18.0	359	1 AG2R_CAVPO	Q94v26 cavia porce

34	320	18.0	370	1 P2Y9_HUMAN	Q99677 homo sapien
35	319.5	18.0	365	1 GP68_HUMAN	Q15743 homo sapien
36	319	17.9	359	1 AG2R_RAT	P25095 rattus norv
37	319	17.9	359	1 AG2S_RAT	P29089 rattus norv
38	318	17.9	359	1 AG2R_MOUSE	P29754 mus musculu
39	318	17.9	361	1 P2Y4_MOUSE	Q91157 mus musculu
40	316.5	17.8	398	1 OPRM_RAT	P33535 rattus norv
41	316	17.8	359	1 AG2S_MOUSE	P29755 mus musculu
42	316	17.8	377	1 APJ_RAT	Q91hg3 rattus norv
43	316	17.8	397	1 PAR2_RAT	Q63645 rattus norv
44	313.5	17.6	380	1 APJ_HUMAN	P35414 homo sapien
45	313.5	17.6	401	1 OPRM_PIG	Q95247 sus scrofa

ALIGNMENTS

RESULT 1
ID P2YC_HUMAN STANDARD: PRT: 342 AA.
AC Q9H244;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE P2Y purinoceptor 12 (P2Y12) (P2Y12 platelet ADP receptor) (P2Y(ADP))
DE (ADP-glucose receptor) (ADPG-R) (P2Y(AC)) (P2Y(cyc)) (P2Y(AC))
DE (SP1999).
GN P2RY12 OR HOKR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21037966; PubMed=11196645;
RA Holopecer G., Jantzen H.-M., Vincent D., Li G., England L.,
RA Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J.,
RA Conley P.B.;
RT "Identification of the platelet ADP receptor targeted by
RT antithrombotic drugs.";
RL Nature 409:202-207(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Hypothalamus;
RX MEDLINE=21269433; PubMed=11104774;
RA Zhang F.L., Luo L., Gustafson E., Lachowicz J., Smith M., Qiao X.,
RA Liu Y.-H., Chen G., Pramanik B., Laz T.M., Palmer K., Bayne M.,
RA Monsie F.J. Jr.;
RT "ADP is the cognate ligand for the orphan G protein-coupled receptor
RT SP1999.";
RL J. Biol. Chem. 276:8608-8615(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=21394281; PubMed=11502873;
RA Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.-I.,
RA Ohishi T., Soga T., Matsushime H., Furuchi K.;
RT "Molecular cloning of the platelet P2Y(AC) ADP receptor:
RT pharmacological comparison with another ADP receptor, the P2Y1
RT receptor.";
RL Mol. Pharmacol. 60:432-439(2001).
RN [4]
RP SEQUENCE FROM N.A.
RA Reinisch R.K., Nothacker H.-P., Wang Z., Zeng J., Ehler F.J.,
RA Clevell O.;
RT "ADP-glucose activates a G-protein coupled receptor and inhibits
RT smooth muscle contractions.";
RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takeasu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";

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RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RP [6]
RN SEQUENCE FROM N.A.
RC TISSUE-Prostate:
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
CC inhibit the adenylyl cyclase second messenger system. Not
CC activated by UDP and GTP. Involved in platelets aggregation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in the platelets, lower
CC levels in the brain. Lowest expressed in the lung, appendix,
CC pituitary and adrenal gland. Expressed in the spinal cord and in
CC the fetal brain.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF313449; AAC49844.1; -
CC EMBL: AF321815; AAK00948.1; -
CC EMBL: AB052684; BAB0824.1; -
CC EMBL: AF310685; AAL32292.1; -
CC EMBL: AB083596; BAB89309.1; -
CC EMBL: BC017898; AAH17898.1; -
CC MIM: 600515; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS: PR00237; GPCR_Rhodopsn.
CC DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
CC DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
CC KM G-protein coupled receptor; Transmembrane; Glycoprotein.
CC FT DOMAIN 1 25
CC TRANSMEM 26 46
CC FT DOMAIN 47 58
CC TRANSMEM 59 79
CC FT DOMAIN 80 99
CC TRANSMEM 100 120
CC FT DOMAIN 121 142
CC TRANSMEM 143 163
CC FT DOMAIN 164 191
CC TRANSMEM 192 212
CC FT DOMAIN 213 233
CC TRANSMEM 234 254
CC FT DOMAIN 255 281
CC TRANSMEM 282 302
CC FT DOMAIN 303 342
CC DISULFID 97 175
CC FT CARBOHYD 6 6
CC FT CARBOHYD 13 13
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 342 AA; 39438 MW; 8553D2746C89176D CRC64;

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Query Match 100.0%; Score 1778; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 1; 5e-112;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 181 EFGLVMEIYNYICQVIFWINEFLIVICYTLITKELYSRYVRGKVPKRVNVEFI 240
DB 181 EFGLVMEIYNYICQVIFWINEFLIVICYTLITKELYSRYVRGKVPKRVNVEFI 240
QY 241 IIAVFICFVPHFARIPYLTSTQRDVFDCAENTLFFVVESTLMTLSNACLDPIYFF 300
DB 241 IIAVFICFVPHFARIPYLTSTQRDVFDCAENTLFFVVESTLMTLSNACLDPIYFF 300
QY 301 LCKSFNSLSMLCKPNSATSLSDNRRKEDQGDPEDEEPM 342
DB 301 LCKSFNSLSMLCKPNSATSLSDNRRKEDQGDPEDEEPM 342

RESULT 2
P2YC_MACFA
ID P2YC_MACFA STANDARD; PRT; 342 AA.
AC 095KC3; 09BGF8;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE P2Y purinoceptor 12 (P2Y12).
GN P2RY12.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Frontal cortex, and Medulla oblongata;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
CC inhibit the adenylyl cyclase second messenger system (by
CC similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AB056385; BAB3041.1; -
CC EMBL: AB062981; BAB60747.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS: PR00237; GPCR_Rhodopsn.
CC PRINTS: PR01569; P2Y12_PRNCPTR.
CC DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
CC DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
CC KM G-protein coupled receptor; Transmembrane; Glycoprotein.
CC FT DOMAIN 1 25
CC TRANSMEM 26 46
CC FT DOMAIN 47 58
CC TRANSMEM 59 79
CC FT DOMAIN 80 99
CC TRANSMEM 100 120
CC FT DOMAIN 121 142
CC TRANSMEM 143 163
CC FT DOMAIN 164 191
CC TRANSMEM 192 212
CC FT DOMAIN 213 233
CC TRANSMEM 234 254
CC FT DOMAIN 255 281
CC TRANSMEM 282 302

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FT DOMAIN 303 342 CYTOPLASMIC (POTENTIAL).
FT DISULFID 97 175 BY SIMILARITY.
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 49 49 I -> T (IN REF. 1: BAB33041).
FT CONFLICT 89 89 A -> T (IN REF. 1: BAB33041).
SQ SEQUENCE 342 AA; 39479 MM; E93FC26BBF5EC4C CAC64;

Query Match 98.3%; Score 1748; DB 1; Length 342;
Best Local Similarity 98.0%; Pred. No. 1.5e-110;
Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MQAVDNLSAGNLSLCRDYKITOVLPFLTYVLFVGLITNGIAMRIFQIRSKSNFI 60
DB 1 MQAIDNLSAGNLSLCRDYKITOVLPFLTYVLFVGLITNSIAMRIFQIRSKSNFI 60
QY 61 IFLNKTVISDLMLTFPFKILSDAKLGAPLRFVCOVSVIFFTMYISISFLGLTI 120
DB 61 IFLNKTVISDLMLTFPFKILSDAKLGAPLRFVCOVSVIFFTMYISISFLGLTI 120
QY 121 DRYKTRPFTSNPKNLGAKILSVIWMFELSLPNMILTNRPDKNVKCKSFLKS 180
DB 121 DRYKTRPFTSNPKNLGAKILSVIWMFELSLPNMILTNRPDKNVKCKSFLKS 180
QY 181 EFGLVMEIIVYICQVIFWIFLYIVCYTLITKELISYVTRGCVGPKRVKVFYI 240
DB 181 EFGLVMEIIVYICQVIFWIFLYIVCYTLITKELISYVTRGCVGPKRVKVFYI 240
QY 241 IIAVEFICFVFHFRARIPYTLISQFADVDCATNENTLFVVKESTLMLSLNCLDPIETFF 300
DB 241 IIAVEFICFVFHFRARIPYTLISQFADVDCATNENTLFVVKESTLMLSLNCLDPIETFF 300
QY 301 LCKSFRLNLSMLKCPNSATSLSODNRKEDGGDPNETPM 342
DB 301 LCKSFRLNLSMLKCPNSATSLSODNRKEDGGDPNETPM 342

RESULT 3
P2YC.MOUSE STANDARD; PRT; 347 AA.
ID P2YC.MOUSE
AC 09CPV9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE P2Y purinoceptor 12 (P2Y12).
GN P2RY12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN RP
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus, and Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Bonfelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guetlich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombereits P.,
RA Notdone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
```

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RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
CC inhibit the adenylyl cyclase second messenger system (By
CC similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AK013804; BAB29000.1; -
DR EMBL; AK014807; BAB29561.1; -
DR EMBL; BC025428; AAH25428.1; -
DR EMBL; BC027381; AAH27381.1; -
DR MGD; MGI:1918089; p2ry12.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCRHOPOPSN.
DR PRINTS; PRO1569; P2Y12PRNCTR.
DR PRINTS; PRO1655; UDPGLUCOSER.
DR PROSITE; PS00237; G-PROTEIN_RECPR_F1_1; FALSE_NEG.
DR PROSITE; PS0262; G-PROTEIN_RECPR_F1_2; 1.
DR K-PROTEIN coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 31
FT TRANSMEM 32 52
FT DOMAIN 53 64
FT TRANSMEM 65 85
FT DOMAIN 86 105
FT TRANSMEM 106 126
FT DOMAIN 127 148
FT TRANSMEM 149 169
FT DOMAIN 170 197
FT TRANSMEM 198 218
FT DOMAIN 219 239
FT TRANSMEM 240 260
FT DOMAIN 261 287
FT TRANSMEM 288 308
FT DOMAIN 309 347
FT DISULFID 103 181
FT CARBOHYD 7 7
FT CONFLICT 3 3
SQ SEQUENCE 347 AA; 39473 MM; F107488E57E025F1 CAC64;

Query Match 87.5%; Score 1555.5; DB 1; Length 347;
Best Local Similarity 88.7%; Pred. No. 1.2e-97;
Matches 299; Conservative 16; Mismatches 21; Indels 1; Gaps 1;

QY 6 NLSAPGNTSLCTRYKITOVLPFLTYVLFVGLITNGIAMRIFQIRSKSNFIIFKN 65
DB 12 NLTSPGNTSLCTRYKITOVLPFLTYVLFVGLITNSIAMRIFQIRSKSNFIIFKN 71
QY 66 TVISDLMLTFPFKILSDAKLGAPLRFVCOVSVIFFTMYISISFLGLITIDRYOK 125
DB 72 TVISDLMLTFPFKILSDAKLGAPLRFVCOVSVIFFTMYISISFLGLITIDRYOK 131
QY 126 TTRPRTSNPKNLGAKILSVIWMFELSLPNMILTNRPDKNVKCKSFLKSEFGY 185
DB 132 TTRPRTSNPKNLGAKILSVIWMFELSLPNMILTNRPDKNVKCKSFLKSEFGY 191
QY 186 WHEIYNYICQVIFWIFLYIVCYTLITKELISYVTRGCVGPKRVKVFYIITAVE 245
DB 192 WHEIYNYICQVIFWIFLYIVCYTLITKELISYVTRGCVGPKRVKVFYIITAVE 251
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QY	246	FICVCPHFPAIPPTLSTQTRVFCPCSTLTFYKCESTMLTSLNACLDPEIFYFLCKSF	309
Db	252	FICVCPHFPAIPPTLSTQTRAVFPCSAENTLFYKCESTMLTSLNACLDPEIFYFLCKSF	3111
QY	306	NSLISMLKCPNSATSLSQDNRRKEODGDPNEETPM	342
Db	312	NSLISMLRCSNS-TSTSGTRKKKGCGGEPSEETPM	347
RESULT 4			
	P2YC_RAT	STANDARD;	PRT; 343 AA.
AC	Q9EPX4;		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	P2Y purinoceptor 12 (P2Y12) (P2Y12 platelet ADP receptor).		
GN	P2RY12.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumleostomi;		
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus		
OX	NCBI_TaxID=10116;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Sprague-Dawley;		
RX	MEDLINE=21037966; PubMed=11916645;		
RA	Hollopeter G., Jantzen H.-M., Vincent D., Li G., England L.,		
RA	Kamakishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J.,		
RA	Conley P.B.;		
RT	"Identification of the platelet ADP receptor targeted by		
RT	antithrombotic drugs."		
RL	Nature 409:202-207(2001).		
CC	-1- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that		
CC	inhibit the adenylyl cyclase second messenger system (by		
CC	similarity).		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	-----		
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CC	use by non-profit institutions as long as its content is in no		
CC	modified and this statement is not removed. Usage by and for comm		
CC	entities requires a license agreement (See http://www.isb-sib.ch/annou		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; AF13450; AAC64945.1; -		
DR	InterPro: IPR000276; GPCR_Rhodopsn.		
DR	Pfam: PF00001; 7tm_1. 1.		
DR	PRINTS: PR00237; GPCRHHODOPSN.		
DR	PRINTS: PRO1564; OGR1RECEPTOR.		
DR	PRINTS: PRO1659; P2Y12PRNCPTR.		
DR	PRINTS: PRO1655; UDPGLUCOSER.		
DR	PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.		
DR	PROSITE: PS50263; G-PROTEIN_RECEP_F1_2. 1.		
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.		
FT	DOMAIN	1	31
FT	TRANSHEM	32	52
FT	DOMAIN	53	64
FT	TRANSHEM	65	85
FT	DOMAIN	86	105
FT	TRANSHEM	106	126
FT	DOMAIN	127	148
FT	TRANSHEM	149	169
FT	DOMAIN	170	197
FT	TRANSHEM	198	218
FT	DOMAIN	219	239
FT	TRANSHEM	240	260
FT	DOMAIN	261	287
FT	TRANSHEM	288	308
FT	DOMAIN	309	343
FT	DISULFID	103	181
FT	CARBOHYD	7	7
N-LINKED (GLCNAC. . .) (POTENTIAL).			

[illegible]

[illegible]

RESULT 6
p2yx_MOUSE

ID	p2yx_MOUSE	STANDARD:	PRF:	338 AA.
AC	Q9ESG6;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	UDP-glucose receptor (G protein-coupled receptor GPR105).			
GN	GPR105.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Lee B.C., Scadden D.T.;			
RT	"7 transmembrane G protein coupled receptor from hematopoietic progenitors."			
RL	Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.			
CC	-1- FUNCTION: Receptor for UDP-glucose coupled to G-proteins (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sdb.ch/announce/ or send an email to license@isb-sdb.ch).			
CC	-----			
DR	EMBL; AF177211; AACG9275.1; -			
DR	MGD; MGI:2155705; Gpr105.			
DR	InterPro: IPR000276; GPCR_Rhodopsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PRO0237; GPCRKHODOPS.			
DR	PRINTS; PRO1569; P2Y12PRNCPT.			
DR	PRINTS; PRO1655; UDPGLUCOSER.			
DR	PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; FALSE_NEG.			
DR	PROSITE; PS50262; G-PROTEIN_RECEP_FL_2; 1.			
KM	G-protein coupled receptor: Transmembrane; Glycoprotein.			
FT	DOMAIN 1 29			
FT	DOMAIN 30 50			
FT	TRANSMEM 51 55			
FT	DOMAIN 56 76			
FT	TRANSMEM 77 96			
FT	DOMAIN 97 117			
FT	TRANSMEM 118 139			
FT	DOMAIN 140 160			
FT	TRANSMEM 161 188			
FT	DOMAIN 189 209			
FT	TRANSMEM 210 234			
FT	DOMAIN 235 255			
FT	TRANSMEM 256 278			
FT	DOMAIN 279 299			
FT	TRANSMEM 300 338			
FT	DOMAIN 339 358			
FT	DISULFID 359 378			
FT	CARBOHYD 379 398			
FT	CARBOHYD 399 418			
SO	SEQUENCE 338 AA; 38861 MW; 4376506522A68A4E CRC64;			
Query Match	41.7%;	Score 741.5;	DB 1;	Length 338;
Best Local Similarity	44.1%;	Pred. No. 3.6e-43;		
Matches 146;	Conservative 69;	Mismatches 109;	Indels 7;	Gaps 3.

4 VDNLTASAGNLSLCRDVKITQVLEPLLYTVLEFGLITNGLAMRFPRIRKSNPTITL 63
1 MNNSTTTPDPNPQGNWNLITKQIIIVLXGWFITGLLNGISGWIEFVPSKSPITVL 60
64 KNTVSDLMILTFSPFKLISDAKLTGPIRFEVCQVTSVIEFTWISISFGLITIDRY 123

RT for platelet activating factor.";
 RL Biochem. Biophys. Res. Commun. 180:105-111(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE=92041873; PubMed=1657923;
 RA Nakamura M., Honda Z., Izumi T., Sakanaka C., Mutoh H., Minami M.,
 Bito H., Seyama Y., Matsumoto T., Noma M., Shimizu T.;
 RT "Molecular cloning and expression of platelet-activating factor
 receptor from human leukocytes.";
 RL J. Biol. Chem. 266:20400-20405(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92250505; PubMed=1374385;
 RA Kunz D., Gerard N.P., Gerard C.;
 RT "The human leukocyte platelet-activating factor receptor. cDNA
 cloning, cell surface expression, and construction of a novel
 epitope-bearing analog.";
 RL J. Biol. Chem. 267:9101-9106(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92347886; PubMed=1322356;
 RA Seyfried C.E., Schwelckart V.L., Godiska R., Gray P.W.;
 RT "The human platelet-activating factor receptor gene (PTAFR) contains
 no introns and maps to chromosome 1.";
 RL Genomics 13:832-834(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=93112021; PubMed=1281995;
 RA Sugimoto T., Tsuchimochi H., McGregor C.G., Mutoh H., Shimizu T.,
 Kurachi Y.;
 RT "Molecular cloning and characterization of the platelet-activating
 factor receptor gene expressed in the human heart.";
 RL Biochem. Biophys. Res. Commun. 189:617-624(1992).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Benai R.H., Debussere M.S., Olson M.S.;
 RL Submitted (xxx-1992) to the EMBL/Genbank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93192035; PubMed=8383507;
 RA Chase P.B., Halonen M., Regan J.W.;
 RT "Cloning of a human platelet-activating factor receptor gene:
 evidence for an intron in the 5'-untranslated region.";
 RL Am. J. Respir. Cell Mol. Biol. 8:240-244(1993).
 CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR. A CHEMOTACTIC
 PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
 MUSCLE CONTRACTILE AND HYPERTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
 ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CALCIUM SECOND MESSENGER SYSTEM.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL, M80436; AAA60001.1; -;
 DR EMBL, M76674; AAA60002.1; -;
 DR EMBL, D10202; BAA01050.1; -;
 DR EMBL, M88177; AAA60214.1; -;
 DR EMBL, S52524; AAB24695.2; -;
 DR EMBL, L07334; AAA60108.1; -;
 DR EMBL, S56396; AAB25755.1; -;
 DR PIR, JH0479; JH0479.
 DR PIR, A40191; A40191.
 DR PIR, A41079; A41079.
 DR Genew, HGNC:9582; PTAFR.

DR MW, 173393; -;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis;
 KM Polymorphism.
 FT DOMAIN 1 16
 FT TRANSMEM 17 38
 FT DOMAIN 39 54
 FT TRANSMEM 55 74
 FT DOMAIN 75 91
 FT TRANSMEM 92 113
 FT DOMAIN 114 133
 FT TRANSMEM 134 155
 FT DOMAIN 156 184
 FT TRANSMEM 185 205
 FT DOMAIN 206 233
 FT TRANSMEM 234 254
 FT DOMAIN 255 276
 FT TRANSMEM 277 296
 FT DOMAIN 297 342
 FT DISULFID 90 173
 FT CARBOHYD 169 169
 FT VARIANT 224 224
 FT VARIANT 338 338
 FT CONFLICT 28 28
 FT CONFLICT 66 66
 FT CONFLICT 95 95
 FT CONFLICT 227 228
 FT CONFLICT 227 228
 FT CONFLICT 247 247
 FT CONFLICT 316 316
 SQ SEQUENCE 342 AA; 39203 MW; 890073C9BBA79228 CRC64;
 Query Match 22.2%; Score 394; DB 1; Length 342;
 Best Local Similarity 32.6%; Pred. No. 6.7e-20;
 Matches 107; Conservative 61; Mismatches 134; Indels 26; Gaps 10;
 QY 11 PONTSLCTRDYKITYTOVLPPLTYVLFVGLTNGLAMRFFQIR--SKSNFI-IFLKNV 67
 DB 3 PDDSHMDESEFRY--LPIIVYSIIFVLGVANGVLMFAFLYPCCKFNEIKIMVNL 60
 QY 68 ISDLMLITLFPFKIISDAKLGCPRTFCVTSVIEFTWYISISGLITIDRYOKT 127
 DB 61 MADMFLFLITLPLMTIVYVYQNGWMLPKFLCNVAGCLFINTYCSVAFGLVITYNRFQAVT 120
 QY 128 RPKFTSNPKNLGAKILSVIV-----AFMFLSLPNMILTRQPRDK---NVKKCSFLK 179
 DB 121 RIKTAQANTRKRGISLSIVWALVGAASYFLIDS---TFTVDSAGSGSVTFC-FEH 176
 QY 180 SEGLVMEIYVYICOVFWINFLVIYCYTLITELYSYVTRNGVGRPKKYNVAVF 239
 DB 177 YEKGSVPVLIHIFVFSFVFLVILFCNLVITRLMQPQOORNAEVRRLAM-VC 235
 QY 240 IIAVFEICFVPHARIPYTLSTRDVFDCAENTLFFVKESTLMLSLNACLDPEYF 299
 DB 236 TYLAFFIICFVHHVAVQLPWTLAEL-GRDQSKFHQAINDAHVTLCLSTNCVLDPVYIC 294
 QY 300 FLCKSFNR-----SLISMLKCPNSAT 320
 DB 295 FLTKKFRKILTEKFSMSSRCKSNATT 322
 RESULT 12
 PAFR_CAVPO STANDARD: PRT; 342 AA.
 ID PAFR_CAVPO
 AC P21556;
 DT 01-MAY-1991 (Rel. 18. Created)
 DT 01-AUG-1991 (Rel. 19, last sequence update)
 DT 01-OCT-1996 (Rel. 34, last annotation update)

```

DE Platelet activating factor receptor (PAF-R).
GN PAFR.
OS Crinia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathia; Cavidae; Cavia.
OX NCBI_Taxid=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=9101726; Pubmed=1846231;
RA Honda Z.-I., Nakamura M., Miki I., Minami M., Watanabe T., Seyama Y.,
RA Okada H., Togh H., Ito K., Miyamoto T., Shimizu T.;
RT "Cloning by functional expression of platelet-activating factor
RT receptor from guinea-pig lung."
RL Nature 349:342-346(1991).
CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC
CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
CC ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56736; CAA40060.1; -.
DR PIR: S13638; S13638.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; transmembrane; glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 16 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 17 38 1 (POTENTIAL).
FT DOMAIN 39 54 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 55 74 2 (POTENTIAL).
FT DOMAIN 75 91 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 92 113 3 (POTENTIAL).
FT DOMAIN 114 133 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 134 155 4 (POTENTIAL).
FT DOMAIN 156 184 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 185 205 5 (POTENTIAL).
FT DOMAIN 206 233 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 234 254 6 (POTENTIAL).
FT DOMAIN 255 276 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 277 296 7 (POTENTIAL).
FT DOMAIN 297 342 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 169 169 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 90 173 BY SIMILARITY.
SQ SSQUNCE 342 AA; 38984 MW; B64133B5A5C87B175 CRC64;
Query Match 22.1%; Score 392.5; DB 1; Length 342;
Best Local Similarity 30.7%; Pred. No. 8,5e-20;
Matches 103; Conservative 66; Mismatches 146; Indels 21; Gaps 9;

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DB 130 TRKGIALSLIVTWAIAAASYFLVMDSTNVNKKASGNTRC-FEHYKSGPVLLIH 188
OY 188 EIVNYICQVI-FWINFLIVICYLLTKELYSYVRTRGVGRKRVNKKVFIIIAVF 246
DB 189 -----ICIVGEFFIVFLILFCNLIYIHTLLRQVKKORNAEV-RRAALMWCVCLAVFV 242
OY 247 ICFVPHFARIPYLLSOTRDVDFDCAENTLFYVESILMLTSLNACDDPFIYFLCSFR 306
DB 243 ICFVPHHVVOLPWTIAEL-GMPPSSNHOAINDAQVTLCLSTNCVDPVYICFLTKRFR 301
OY 307 NSLISMLCKPNSATSLSDNKRKQDGDGPNEETPM 342
DB 302 KHLSEKLNIMMSOKCSRVTDTGTMAIPINHFPV 337

RESULT 13
EB12_HUMAN
ID EB12_HUMAN STANDARD; PRT; 361 AA.
AC P32249;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE EBV-induced G protein-coupled receptor 2 (EBI2).
GN EB12.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93188173; Pubmed=8383238;
RA Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,
RA Kleif E.;
RT "Epstein-Barr virus-induced genes: first lymphocyte-specific G
RT protein-coupled peptide receptors."
RL J. Virol. 67:2209-2220(1993).
CC -1- FUNCTION: ONCPHAN RECEPTOR. PROBABLE MEDIATOR OF EBV EFFECTS ON B
CC LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -1- TISSUE SPECIFICITY: B-LYMPHOCYTE CELL LINES.
CC -1- INDUCTION: BY EBV.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L08177; AAA35924.1; -.
DR PIR: B45680; B45680.
DR Genew: HGNC:3128; EB12.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; transmembrane; glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 32 57 1 (POTENTIAL).
FT DOMAIN 58 77 2 (POTENTIAL).
FT TRANSMEM 78 95 2 (POTENTIAL).
FT DOMAIN 96 105 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 106 127 3 (POTENTIAL).
FT DOMAIN 128 149 4 (POTENTIAL).
FT TRANSMEM 150 168 4 (POTENTIAL).
FT DOMAIN 169 192 5 (POTENTIAL).
FT TRANSMEM 193 215 5 (POTENTIAL).
FT DOMAIN 216 241 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 242 265 6 (POTENTIAL).

```

CC	-----
DR	EMLL, AB052662; BAB0817.1; -
DR	InterPro: IPR000276; GPCR_Rhodopsin.
DR	Pfam: PF00001; 7tm_1; 1.
DR	PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; FALSE_NEG.
DR	PROSITE: PSS0262; G-PROTEIN_RECEP_FL_2; 1.
KW	G-protein coupled receptor; Transmembrane, glycoprotein, EXTRACELLULAR (POTENTIAL).
FT	DOMAIN 1 43
FT	TRANSSEM 44 64
FT	DOMAIN 65 73
FT	TRANSSEM 74 94
FT	DOMAIN 95 124
FT	TRANSSEM 125 145
FT	DOMAIN 146 154
FT	TRANSSEM 155 175
FT	DOMAIN 176 205
FT	TRANSSEM 206 226
FT	DOMAIN 227 246
FT	TRANSSEM 247 267
FT	DOMAIN 268 287
FT	TRANSSEM 288 308
FT	DOMAIN 309 345
FT	DISULFID 112 188
FT	CARBOHYD 20 20
FT	CARBOHYD 29 29
FT	CARBOHYD 177 177
FT	CARBOHYD 184 184
SQ	SEQUENCE 345 AA; 39410 MM; SD1BJFB89B95905 CRC64;
Query Match	20.68; Score 367; DB 1; Length 345;
Best Local Similarity	29.08; Pred. No. 4,4e-18;
Matches 93; Conservative 72; Mismatches 134; Indels 22; Gaps 9;	
QY	1 MQADVNLTSASGNTSLCRDYKRTQVLEPLLYTVLFEGFLTNGLAMRIFQIRKSNEFI 60
Dd	17 MEPNSTLCNHNHNSNSCTTENK--REFPIYLVLFTMGALONGSIVYELKPKAKTSV 74
QY	61 -IFLNKTVISDLMLILTPPKI----ISDAKLGTGRFTFCQVTSVIFYFTYISIF 114
Dd	75 NVFMNLAISSLDFLTITLPFRVDYLRSGNMIFGDT-----CRMYSMTVMNYSSIFY 129
QY	115 LGLITIDRYQKTTREPKFSKNRNLLGAATLSVVAWFNFLLSLPMILITNRQPRKNVK 174
Dd	130 LTIVSVVEFLTAVHPRLHTTHSIKNAMIILOGVI--IFIMASSVTLLKNSSECDQNTL 187
QY	175 CSFLSKSERGLWMHEIVNICQVI-EWINEFLAYVCYLITKELYRSVYRTGVCGKVPKK 233
Dd	188 CLELNSN-KVTKRLKMNVALVCGFVLDPFGTLISCTYLILTRALLKVEVPESGL-RLSHRK 245
QY	234 VNVKVFIIIAVEFLICFVPEHFARIPYTLISQTRDVEDCAETNALTFFYKESTLMTLSNAQL 293
Dd	246 ALITYIALIIFLICFLDYHLVLRTHILEMKAD----CKKRRLRAVAVTALAANAANSCF 301
QY	294 DPFIYFLCKSPFNLSLSMLK 314
Dd	302 NPFLYYFAGENFKDKLSALR 322
RESULT 15	
PAFR_MOUSE	STANDARD; PRT; 341 AA.
ID	PAFR_MOUSE
AC	O62035;
DT	15-JUL-1998 (Rel. 36, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DE	15-JUL-1998 (Rel. 36, Last annotation update)
GN	Platelet activating factor receptor (PAF-R).
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX	NCBI_TaxID=10090;
NN	[1]
RP	SEQUENCE FROM N.A.

RC STRAIN-129/SV:
 RA MEDLINE-96239129; PubMed-8670084;
 RA Ishii S., Matsuda Y., Nakamura M., Waga I., Kume K., Izumi T.,
 RA Noma M., Shmizu T.;
 RT "A murine platelet-activating factor receptor gene: cloning,
 RT chromosomal localization and up-regulation of expression by
 RT lipopolysaccharide in peritoneal resident macrophages.";
 RL Biochem. J. 314:671-678(1996).
 CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC
 CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
 CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
 CC ACTION VIA A G PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: D50872; BAA09468.1; -
 DR MGD: MGI:106066; Pfaff.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN 1 16
 FT TRANSMEM 17 38
 FT DOMAIN 39 54
 FT TRANSMEM 55 74
 FT DOMAIN 75 91
 FT TRANSMEM 92 113
 FT DOMAIN 114 133
 FT TRANSMEM 134 155
 FT DOMAIN 156 184
 FT TRANSMEM 185 205
 FT DOMAIN 206 233
 FT TRANSMEM 234 254
 FT DOMAIN 255 275
 FT TRANSMEM 276 295
 FT DOMAIN 296 341
 FT CARBOHYD 4 4
 FT CARBOHYD 159 169
 FT DISULFID 90 173
 SQ SEQUENCE 341 AA; 39148 MW; CAA8CDDBD8D26897 CRC64;
 Query Match 20.6%; Score 366; DB 1; Length 341;
 Best Local Similarity 29.9%; Pred. No. 5e-18;
 Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;
 Oy 20 DYKTTQVLEFLLYVLEFVGLITNGLANRIFQI--RSKSNFI--LEKNVVISDLMLIT 76
 Db 10 DSEFRYTLFPIYVSIFLIGVANGYVLMVFNLPYSKLEIKIFMVLTMADLLFLIT 69
 Oy 77 FPFKILSAKIGPLRFGVQVSIVFYFTMYISISFLGLITDRYOKTRPFTSNPK 136
 Db 70 LPLMTVYYVYNEGDMILPFLCNVAGCLFEINFGYSAFLGVITNRYQAVAVPIKTAQAT 129
 Oy 137 NLGAKILSVYVAFM-----FLSLPMILITNROPDRKNKCSFLKSEFG--LVWHE 188
 Db 130 TRKRGISLSLTIWYSIVATATSTNLVPKDGSGNITRCPEHEPEYVPLIVVHV 189
 Oy 189 IVNYICQYIEMINFLI-VIVCYTLITKELYSYVTRGVGVPRKRVKVFIIIAVFEI 247
 Db 190 FIACCFVLFPLIFCNVLIHTLITLQPMRQ--RKAGV---KRALMNVCTVLAVFII 243
 Oy 248 CFVPHFARIRITYTISQTDVDCIAENTLIFYKESTLMLTSLMACLDPIFYFLCKSFRN 307

Db 244 CFVPHVVOLEPMTLAEIG--YQNFHOAINDAHOITLCLSTNCVLDVPIYCFITKFRK 301
 Oy 308 -----SLISMLKCPNSATS 321
 Db 302 HISEKFTYMRSSRC-SRATS 321

Search completed: December 6, 2002, 10:04:55
 Job time : 35 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 6, 2002, 10:04:12 ; Search time 101 Seconds

(without alignments)
697.704 Million cell updates/sec

Title: US-09-835-922-2

Perfect score: 1778

Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SQDNKKKQDGGDPNETTPM 342

Scoring table:

BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	829	46.6	333	4	Q9BPV8
2	823	46.3	333	4	Q8TUD7
3	794	44.7	337	11	Q9D8T2
4	699.5	39.3	358	4	Q96JZ8
5	694.5	39.1	358	4	Q9B721
6	685.5	38.6	359	11	Q99MT7
7	559	31.4	228	6	Q9BE53
8	553.5	31.1	269	4	Q9BXC2
9	448	25.2	176	4	Q9B6T1
10	388.5	21.9	342	6	Q9RTY5
11	387.5	21.8	342	6	Q9GK76
12	368.5	20.7	296	6	Q9TYV6
13	365	20.5	342	6	Q9XSD4
14	356	20.0	374	13	Q57466
15	343	19.3	359	13	Q9PYV7
16	338	19.0	359	6	Q9N0U1

17	336	18.9	309	11	Q8R5Z8	Q8R5Z8 mus musculus
18	322	18.1	359	11	Q9EPF3	Q9EPF3 cavia porce
19	321	18.1	359	6	Q9GLN9	Q9GLN9 pan troglod
20	318.5	17.9	399	11	Q8R3I1	Q8R3I1 mus musculus
21	318	17.9	359	4	Q8TBK4	Q8TBK4 homo sapien
22	314	17.7	400	6	Q95M54	Q95M54 macaca fasc
23	309	17.4	358	13	Q9PUA0	Q9PUA0 acipenser r
24	309	17.4	454	4	Q9H573	Q9H573 homo sapien
25	307	17.3	359	11	Q9EGR9	Q9EGR9 meriones un
26	304.5	17.1	390	10	Q8V171	Q8V171 mus musculus
27	304.5	17.1	391	10	Q8V170	Q8V170 mus musculus
28	304.5	17.1	393	11	Q9R1M0	Q9R1M0 mus musculus
29	304.5	17.1	401	11	Q9R1P9	Q9R1P9 mus musculus
30	304.5	17.1	409	11	Q8V169	Q8V169 mus musculus
31	304.5	17.1	438	11	Q9R0D1	Q9R0D1 mus musculus
32	304.5	17.1	444	11	Q9JY14	Q9JY14 mus musculus
33	301.5	17.0	377	13	Q98U14	Q98U14 brachydanio
34	301.5	17.0	390	13	Q8Q6G4	Q8Q6G4 carassius a
35	300	16.9	384	13	Q98UH1	Q98UH1 brachydanio
36	299.5	16.8	352	6	Q9TV45	Q9TV45 cercopithec
37	298	16.8	358	13	Q9YGC3	Q9YGC3 xenopus lae
38	297.5	16.7	339	6	Q9TUS5	Q9TUS5 papio cynoc
39	297	16.7	352	6	Q9TV47	Q9TV47 cercopithec
40	296.5	16.7	361	11	Q8VHP3	Q8VHP3 cavia porce
41	294	16.5	343	11	Q9QW32	Q9QW32 rattus sp.
42	293.5	16.5	352	6	Q9TV43	Q9TV43 cercopithec
43	293	16.5	362	11	Q9JLZ0	Q9JLZ0 rattus norv
44	292.5	16.5	352	6	Q9TS07	Q9TS07 cercopithec
45	291.5	16.4	339	6	Q9TSN3	Q9TSN3 macaca fasc

ALIGNMENTS

RESULT 1						
Q9BPV8		PRELIMINARY:	PRT:	333 AA.		
AC	Q9BPV8:					
DT	01-JUN-2001 (TREMBLrel. 17, Created)					
DT	01-JUN-2001 (TREMBLrel. 17, last sequence update)					
DT	01-JUN-2002 (TREMBLrel. 21, last annotation update)					
DE	Putative G-protein-coupled receptor FKSG77 (G-protein coupled receptor GPR86) (G protein-coupled receptor)					
DE	GPR86)					
GN	FKSG77 OR GPR86 OR GPR94.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
OC	NCBI_TaxID=9606;					
OX	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=HEART;					
RA	Wang Y., Gong L.;					
RT	"Molecular cloning of FKSG77, a novel gene encoding a putative G-					
RT	protein-coupled receptor.";					
RL	Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE-21172992; PubMed-11273702;					
RA	Wittenberger T., Schaller H.C., Hellbrand S.;					
RT	"An expressed sequence tag (est) data mining strategy succeeding in					
RT	the discovery of new G-protein coupled receptors.";					
RL	J. Mol. Biol. 307:799-813(2001).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE-21458557; PubMed-11574155;					
RA	Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantli W.B., Arkhltko O.,					
RA	Lewis T., Evans J.F., George S.R., O'Dowd B.F.;					
RT	"Discovery and mapping of ten novel G protein-coupled receptor					
RT	genes.";					
RL	Gene 275:83-91(2001).					
RN	[4]					
RP	SEQUENCE FROM N.A.					

Query Match	Best Local Similarity	46.6%	Score 829;	DB 4;	Length 333;
Matches 155; Conservative	49.1%	Pred. No. 7e-66;	Mismatches 102;	Indels 2;	Gaps 1;
DB	17	CTRDYKTKQVLEPFLYVLEFVGLITNGLANRIFQIRSKSNFIILKNTVISDLMLIT	76		
QY	17	CTRDYKTKQVLEPFLYVLEFVGLITNGLANRIFQIRSKSNFIILKNTVISDLMLIT	76		
DB	15	CPDRRIYQVLEFALPYVFLTGILNLMLALVFNHPISSPFILYKNTVLADLIMFLM	74		
QY	77	FPFIIISAKKGTGTRFVCOVSVITFYFYMYISISFLGLITTDRIYQKTTPEFKTSNK	136		
DB	75	LPEFIILSSHLAPWOLRAFCVCRFSSVITYETWVGIVLGLIATFRFLKIIPPLRNFILK	134		
QY	137	NILGAKISVYIMAFMFLSLPNMLITNRQPRDKNVKCSFLKSEGLVWHEIYVICOV	196		
DB	135	KPVRAKYVSIITWFLFLFISLPMILMSKKEATPSSVKKCAISLKGSLGKLNHOMVNNICQF	194		
QY	197	IFWINEFLIVCYTTLITRELYRSYVTRGVGKVPKKVNVKVFIIIAVFFICVFPFHAR	256		
DB	195	IFWTFVILMELFVYVYIAKRYVDSYKRSKDKRNNKKLEGKVFVVAVFVFCADPHFAR	254		
QY	257	IPYILSQRDVFDCAENTLIFYVKESTIMLSLNCADPFIYFLFCKSRNLSIMLKP	316		
DB	255	VPHYHSQNNNTDCLRLQNLQFLAKETFLFLAATNLCMDPLIYFLCKPTEKTEPCMO--G	312		
QY	317	NSATSLSDNNRKKED	332		
DB	313	RKTASSQENHSSQTD	328		
RESULT 2					
Q8FTD07					
ID	O8RD07	PRELIMINARY:	PRT:	333 AA.	
AC	O8RD07;				
DT	01-JUN-2002 (TREMBLrel. 21, Created)				
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Puative G-protein coupled receptor.				
GN	GPCR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid:9606;				
RP	SEQUENCE FROM N.A.				
RA	Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;				
RT	"Identification of G protein-coupled receptor genes from the human				
RT	genome sequence."				
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: AB083597; BAB89310.1; -				
KM	Receptor.				
SO	SEQUENCE	333 AA;	38440 MW;	F234ABBS0016DF34 CRC64;	

QY	17	CTPQKTKTQVLPFLYLVYVFFGVLTGMLRFFOLRKSNSNIFLTKVTISDLMILT	76
Db	15	CPROTRIQVQLPALYLVYVELTGLNTLALNFVHIIPSSFTIYILKNTIYADLMITLM	74
QY	77	EPFKILSDAKLGTGPLTEFCQVTSVIEFTMYISISFGLTITDXYOKTTPRFTSNPK	136
Db	75	LPFKILSDSHLAPQULAFPCRESSVYFETMYGVILLGLAFDRFLKIIPRLRIIFLK	134
QY	137	NLFAKILTSVYANFMFLSLPMLNITLRNPDRKANKKCSFLKSEGLGWMHEIVATCOV	196
Db	135	KPVAKTAVYLFIEHFEFLFISIPNTLISNKEATPSSVASCASLGLGLKWMHOMVNICOE	194
QY	197	IFWIFNLIVYCYTLITNKELYSRVTRGVGKVPKRKNVKNVFIIITAVEFICFVPHFAR	256
Db	195	IFWTFVILMLAVEYVYIAKVKYDYSRKSKSDKRNKNNKKLEGVVYAVFVCFAPHFHAR	254
QY	257	IPYTLISOTRDVEFDCATANTLFFYKKESTLMTLSINACLDPIFYIFFLCKSRNSLISMLCKP	316
Db	255	VPHYSTSTNNKTDCRLONOFIAPKETTFLTAANVICMDPLITYIFLCKKTEKPLCMQO-G	312
QY	317	NSATSLSQDNRRKEOD 332	
Db	313	RKTASSQENHSSQTD 328	
RESULT 3			
ID	Q9D812	PRELIMINARY;	PRT; 337 AA.
AC	Q9D812;		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2002 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	2010001L06RIK protein.		
GN	GPR86 OR 2010001L06RIK.		
OS	Mus musculus (mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
CX	NCBI_TaxID-10090;		
RA	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-C57BL/6J; TISSUE-SMALL INTESTINE;		
RX	MEDLINE-21085660; PubMed-11217851;		
RA	Kawai J., Shingawa A., Shibata K., Yoshino H., Itoh M., Ishi Y.,		
RA	Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,		
RA	Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,		
RA	Sato T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,		
RA	Kado T., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Glasl C., King B., Kochwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Schirral L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Mashio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gunstinction S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Saito K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RL	Nature 409:685-690(2001).		
DR	EMBL: AK008013; BAB25409.1; -		
DR	MGI: 1921441; Gpr86		
DR	InterPro: IPR000276; GPCR_Rhodpsn.		
DR	Pfam: Pf00001; 7tm_1; 1.		
DR	PRINTS: PR00237; GPCRHOOPS.		
DR	PRINTS: PR01655; UDPGLUCOSER.		
DR	PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.		
DR	PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.		
QY	SEQUENCE 337 AA; 38693 MW; 2C1A76FBFB9305EA CRC64;		

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Query Match          44.7%; Score 794; DB 11; Length 337;
Best Local Similarity 45.9%; Pred. No. 9.1e-63;
Matches 151; Conservative 63; Mismatches 111; Indels 4; Gaps 3;

OY 6 NLTSPG--NTSLCTRDYKITOVLPFLTYVLFVGLITNGLAMRIFFQIRKSNFIIFL 63
DB 6 NTGMOGRNKSRCRDRMTOLPFLTYVLFVGLITNGLAMRIFFQIRKSNFIIFL 65
OY 64 KNTVSDLMILTFPPKILSDAKLGTPRTFVCQVTSVIEFYEMYSISFGLITIDRY 123
DB 66 KNTLVADLIMLTFPKILSDSHLAPMQLRGVCTLSVFEYEMYSISFGLITIDRY 125
OY 124 QKTTPERTSNPKNLGAKILSVIWAFFELSLDPMILITNRPDKNVKCSFKSEFG 183
DB 126 LKIIPFRTKTEPKTAPAKTAVTSISVMSLFISLPMILITNRPDKNVKCSFKSEFG 184
OY 184 LVMHEIVNYICOVITWIMFLIYVCTLTITKELYSYVTRGVGKPVKVFIIIA 243
DB 185 LVMHGVVSHTCOLIMAFVILMLFLYAVITKKNVSYKRFKSDS--RHKREVKVFIIWA 243
OY 244 VEFICFVPHFARIPYITLSQTRDVEDCTAENTLFYVKESTIMLISLNACLDPFIYFICK 303
DB 244 VEFVGFARLHPRIPIYITLSQTRNKTDCRLNQLFLAKGATLFLATINICMDPLIITILCK 303
OY 304 SFRNSLJMLKCPNSATLSLSDNRKKEOD 332
DB 304 KFTOKVPCVRWGKARTAGSSEDDHSSQTD 332

RESULT 4
OY 096J28 PRELIMINARY; PRT; 358 AA.
AC 096J28;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CDNA FLJ11878 f1s, clone PLACE1003238, weakly similar to probable G
DE protein-coupled receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isegai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosogi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Yamamoto J., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Niimura K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027784; BAB5366.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01569; P2Y12PRNCPTR.
DR PRINTS; PR01655; UDPGLUCOSER.
DR PROSITE; PS00237; G_PROTEIN_RECPEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECPEP_F1_2; 1.
KW SEQUENCE 358 AA; 41462 MW; 7822700C8E3CC7E9 CRC64;

Query Match          39.3%; Score 699.5; DB 4; Length 358;
Best Local Similarity 42.6%; Pred. No. 2.4e-54;
Matches 140; Conservative 67; Mismatches 113; Indels 9; Gaps 5;

OY 6 NLTSPG--NTSLCTRDYKITOVLPFLTYVLFVGLITNGLAMRIFFQIRKSNFIIFL 64
DB 25 NNSDGPGRKNTVL--HNEDRTIVLPVLLIFVASILNGLAWIFPHIRNKTSTFIYFLK 81
OY 65 NTVISDLMLTFPPKILSDAKLGTPRTFVCQVTSVIEFYEMYSISFGLITIDRY 124
DB 65 NTVISDLMLTFPPKILSDAKLGTPRTFVCQVTSVIEFYEMYSISFGLITIDRY 124

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DB 82 NTVADLIMLTFPPKILSDAKLGTPRTFVCQVTSVIEFYEMYSISFGLITIDRY 141
OY 125 KTRPFPKTSNPKNLGAKILSVIWAFFELSLDPMILITNRPDKNVKCSFKSEFG 184
DB 142 KYVRFPGSRRMNTIFTKVLSVCVAVIWAFLSPHILITNGOPTEDNHDCKSLSPICV 201
OY 185 VMEHIVNYICOVITWIMFLIYVCTLTITKELYSYVTRGVGKPVK--KVNKVFIIIA 243
DB 202 KMTAVTVYVNSCLFVAVALIYILGCIYAIISRYIHK--SNQFISQSSRRKRNQSIYVVA 259
OY 244 VEFICFVPHFARIPYITLSQTRDVEDCTAENTLFYVKESTIMLISLNACLDPFIYFICK 303
DB 260 VEFTELPHLCRIPIFTSHDLRLDESQKILLYCKEITLFLSACNVCNCPDIYIFMCR 319
OY 304 SFRNSLJ--SMLKCPNSATLSLSDNRKKE 330
DB 320 SFRRLFKKSNIRTSSEISRSIQSVRSR 348

RESULT 5
OY 09BY21 PRELIMINARY; PRT; 358 AA.
AC 09BY21;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Orphan G protein-coupled receptor 87.
DE GPR87 OR GPR95.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21172992; PubMed=11273702;
RA Wittenberger T., Schaller H.C., Hellebrand S.;
RT "An expressed sequence tag (est) data mining strategy succeeding in
RT the discovery of new G-protein coupled receptors.";
RL J. Mol. Biol. 307:799-813(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=21458357; PubMed=11574155;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanli W.B., Arkhilo O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor
RT genes.";
RL Gene 275:83-91(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF237763; AAK01858.1; -
DR EMBL; AF411114; AAL26485.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PRINTS; PR01655; UDPGLUCOSER.
DR PROSITE; PS00237; G_PROTEIN_RECPEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
KW SEQUENCE 358 AA; 41435 MW; FDI157295B5D10F CRC64;

Query Match          39.1%; Score 694.5; DB 4; Length 358;
Best Local Similarity 42.2%; Pred. No. 6.8e-54;
Matches 139; Conservative 68; Mismatches 113; Indels 9; Gaps 5;

OY 6 NLTSPG--NTSLCTRDYKITOVLPFLTYVLFVGLITNGLAMRIFFQIRKSNFIIFL 64
DB 25 NNSDGPGRKNTVL--HNEDRTIVLPVLLIFVASILNGLAWIFPHIRNKTSTFIYFLK 81
OY 65 NTVISDLMLTFPPKILSDAKLGTPRTFVCQVTSVIEFYEMYSISFGLITIDRY 124
DB 82 NTVADLIMLTFPPKILSDAKLGTPRTFVCQVTSVIEFYEMYSISFGLITIDRY 141
OY 125 KTRPFPKTSNPKNLGAKILSVIWAFFELSLDPMILITNRPDKNVKCSFKSEFG 184

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Db 142 KVKPFGDSRMTSTFTKRVLSVCVMVIMAVLSLPNILLTGQPEDNIDHCSKISPLGV 201
 185 VMHEIVYICQVIFWIFLVIYCYTLITKELYSYVTRGVGKPRK-KYNAVFTIIA 243
 202 KMHDAVTVYVASCLEFVAVLILGCIYIAISRIHKS--SRQFISSSKRRKHNSIRVVA 259
 244 VFICFVPHFARIPYLTSGTRDVFCTAENTLFYKVESTIMLTSLNACLDPIFYFLCK 303
 260 VFETCFPLPHLCRIPTFPFTHDLRLDESQKILYCKEITLFLSACVNCIDPIYFPMCR 319
 QY 304 SFRNSLT--SMKCPNATSLSDNRKE 330
 Db 320 SFSRLEKKSNIPTRSSEIRSLQSVRSR 348

RESULT 6

099MT7 PRELIMINARY; PRT; 359 AA.
 AC 099MT7;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE G-protein coupled receptor GPR87.
 GN GPR87.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21172992; PubMed=11273702;
 RA Wittenberger T., Schaller H.C., Hellebrand S.;
 RT "An expressed sequence tag (est) data mining strategy succeeding in
 the discovery of new G-protein coupled receptors.";
 RL J. Mol. Biol. 307:799-813(2001).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF295366; AAK01866.1; -;
 DR MGD: MGI:1934133; Gpr87.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PRINTS: PR01655; UDPGLUCOSER.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 KM G-protein coupled receptor; glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 359 AA; 41462 MW; 2EB313C273FECDA CRC64;

Query Match 38.6%; Score 685.5; DB 11; Length 359;
 Best Local Similarity 41.7%; Pred. No. 4.3e-53;
 Matches 136; Conservative 65; Mismatches 120; Indels 5; Gaps 3;

QY 8 TSAAGNTSLCTROKIVQVFLPIYTLFVGLTNGLAMIFQISKSNFIIFLKNV 67
 Db 26 STSGHGKSNSTLHNFEDTILPVLIVIVASILLNGLAVIFPHIRNKTSIFILKNIV 85
 QY 68 ISDLMLTFPEFKILSDAKLGTGPLRTFVCOVTVIYFTWYISISFLGLTIDRYOKT 127
 Db 86 VADILMLTFPRIVRAGGPMWFEFILLCRYSVLFYANNYTSIVLGLSVDRILKVV 145
 QY 128 RPEFTSNPKNLGAKIISVIAWFMFLISLPMILNROPDRKNVCKCSFLKSEGLVMH 187
 Db 146 KPFDSHMYSTTFKVLSCVMVIMAILSLPNILITFNGOPKRENIHDMKLSPLGAKMH 205
 QY 188 EIVNYICQVIFWIFLVIYCYTLITKELYSYVTRGVGKPRK-KYNAVFTIIAVEF 246
 Db 206 MAVTVYVSCLEFVAVLILGCIYIAISRIHKS--SRQFISQSSKRRKHNSIRVVAVF 263
 QY 247 ICEVPHFARIPYLTSGTRDVFCTAENTLFYKVESTIMLTSLNACLDPIFYFLCKSR 306
 Db 264 TCFPLPHLCRIPTFPFTHDLRLDESQKILYCKEITLFLSACVNCIDPIYFPMCRSFS 323

QY 307 NSLT--SMKCPNATSLSDNRKE 330
 Db 324 RFLFKSNIRTRSEIRSLQSVRSR 349

RESULT 7

09BE53 PRELIMINARY; PRT; 228 AA.
 AC 09BE53;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=FRONTAL CORTEX;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Tero K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 libraries.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB056816; BAB39342.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PRINTS: PR01655; UDPGLUCOSER.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN.1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 SQ SEQUENCE 228 AA; 26356 MW; 47907F5DBEED22C CRC64;

Query Match 31.4%; Score 559; DB 6; Length 228;
 Best Local Similarity 46.7%; Pred. No. 4.9e-42;
 Matches 105; Conservative 40; Mismatches 78; Indels 2; Gaps 1;

QY 108 MYISIFGLTIDRYOKTTPRFTSNPKNLGAKIISVIAWFMFLISLPMILNROP 167
 Db 1 MYGVIVLGLIAFDRLKIITPLKNIPLFKTVKTYSVFWSFFFLSLPMLNSKEA 60
 QY 168 RDKNVKCSFLKSEGLWMEIVYICQVIFWIFLVIYCYTLITKELYSYVTRGVG 227
 Db 61 TPSSVKKCASLKGVLGKMHQIVNNISOFIRWTFVLVLVYVIAKKVDSYKSKSD 120
 QY 228 KVPKKNVAVKFIITIAVFICFVPHFARIPYLTSGTRDVFCTAENTLFYKVESTIMLT 287
 Db 121 RKNKKLEGKVVAVVAVFVCFADFHTRPVYTSQTNKTKDRIQNLFIKETTFLA 180
 QY 288 SLNACLDPIFYFLCKSPRNSLISMLKCPNATSLSDNRKEED 332
 Db 181 ATNLCMDPLIYIFLCKKFTKLPCKRGKRTIAS--SQENSSQTD 223

RESULT 8

09BXC2 PRELIMINARY; PRT; 269 AA.
 AC 09BXC2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative G-protein-coupled receptor FKS678 (G protein-coupled receptor
 87).
 GN FKS678.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;

Db 175 EHYKSGIPVLTITIFVSEFVFLIILFCNLIIIRLLTQQVOIQRMNAVKKRRALMM- 233
 QY 238 VETIIAVFICFVPEFHARIPYLTISQTRDVEDCAENTLEFVKSTLMTSLNCLDFEI 297
 Db 234 VCVTLAVFIICFVPHHVLQVLPMTLAEI-GFODTDFHOAINDAHOVTLCLLSTNCVLDPII 292
 QY 298 YFELCKSFRRNSLSML-----KCPNSATS 321
 Db 293 YCFLETKRKRHLTKELYSMRSRKC-SRATS 322

RESULT 11

Q9GK76 PRELIMINARY; PRT; 342 AA.
 AC Q9GK76
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE Platelet-activating factor receptor.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang W., Diehl J.R., Plumi F.;
 RT "Partial Sequence of Caprine Platelet-Activating Factor Receptor
 RT Gene."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF020274; AAC39982.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR01559; DDEFYANTGEN.
 DR PROSITE: PS00237; GPCRHHODOPS.
 DR PROSITE: PS00237; G_PROTEIN_RECCEP_F1_1; UNKNOWN_1.
 DR PROSITE: PS0262; G_PROTEIN_RECCEP_F1_2; 1.
 DR KMW Receptor.
 SQ SEQUENCE 342 AA; 39612 MW; 39D9379AED60FDAE CRC64;

Query Match 21.8%; Score 387.5; DB 6; Length 342;
 Best Local Similarity 30.4%; Pred. No. 1.3e-26;
 Matches 102; Conservative 66; Mismatches 127; Indels 41; Gaps 11;

QY 11 PGNTSLCTRDYKTIQVLEPILYVLFVGLITNGIAMRIEFOIRKSNF---IIFLKNTV 67
 Db 3 PNNSEFRVDSERYT--LEPIFYSIIVGLVANGVYLVAFRLVPSKKFNEIKIFMWLT 60
 QY 68 ISDLMLITFPFKILSDAKLCTGPRFVQVTSVIFFTWYISISFLGLITDRYQKTY 127
 Db 61 MADLFLFVTLPLMTVYVYNOGDMILPKFLCLACGFEFFINTYCSVAFLAVTYNRQAVT 120
 QY 128 RPFKTSNPKNLGAKILSVIVM-----AFMFLSLPNNMLTNRQPR--DKNVKKCSF 177
 Db 121 RPIITTAQATTRKRGFLSLIIWVSIVGAASFFVLD-----STNSEPKKSGSNTTRC-F 174
 QY 178 LKSEGLWMEIVNYICOVIFWIMNELIVYCYLTITKELYSYVTRGVGKVPKKVAVK 237
 Db 175 EHYKSGIPVLTITIFVSEFVFLIILFCNLIIIRLLTQQVOIQRMNAVKKRRALMM- 233
 QY 238 VETIIAVFICFVPEFHARIPYLTISQTRDVEDCAENTLEFVKSTLMTSLNCLDFEI 297
 Db 234 VCVTLAVFIICFVPHHVLQVLPMTLAEI-GFODTDFHOAINDAHOVTLCLLSTNCV 292
 QY 293 YFELCKSFRRNSLSML-----KCPNSATS 321
 Db 288 LDPITTCFLTKRKRHLTKELYSMRSRKC-SRATS 322

RESULT 12
 Q9TTY6 PRELIMINARY; PRT; 296 AA.
 ID Q9TTY6

AC Q9TTY6;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DE Platelet-activating factor receptor (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang W.S., Diehl J.R., Murphy K.E.;
 RT "Partial Sequence of Canine Platelet-Activating Factor Receptor
 RT Gene."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF186831; AAF01435.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPS.
 DR PROSITE: PS00237; G_PROTEIN_RECCEP_F1_1; UNKNOWN_1.
 DR PROSITE: PS0262; G_PROTEIN_RECCEP_F1_2; 1.
 DR KMW Receptor.
 FT NON_TER 1 1
 FT NON_TER 296 296
 SQ SEQUENCE 296 AA; 33902 MW; 5494C0771C45E101 CRC64;

Query Match 20.7%; Score 368.5; DB 6; Length 296;
 Best Local Similarity 29.5%; Pred. No. 5.4e-25;
 Matches 90; Conservative 66; Mismatches 124; Indels 25; Gaps 7;

QY 20 DYKITQVLEPILYVLFVGLITNGIAMRIE--FOIRKSNFIIIFLKNVISDLMLIT 76
 Db 2 DSERYTEFPIYVSIIFVGLVANSYVLMFACLPYSKKLEIKIFMWNLTMADLFLYT 61
 QY 77 PPFILSDAKLCTGPRFVQVTSVIFFTWYISISFLGLITDRYQKTYRPRKTSNPK 136
 Db 62 LPLMTIYHNOGNMILDSFLCNLAGCEFFINTYCSVAFLAVTYNRQAVTPIKTAQAT 121
 QY 137 NLGAKILSVIVM-----AFMFLSLPNNMLTNRQPRDNVKKCSFLKSEFLWHEI 189
 Db 122 TRKRGFLVSLIVVAIYAAASYFLIDSTNVPS--KSGSNTTRC-FEHKESVAVLI 178
 QY 190 VNYICQVIFWIMNELIVYCYLTITKELYSYVTRGVGKVPKKVAVNYIIVFICF 249
 Db 179 VHVIFVGLFVFLIFFCNVIIIRLLMOPVQLQHNAEYRRALMM-VCTVLAVFIVCF 237
 QY 250 VPFHARIPYLTISQTRDVEDCAENTLEF---VKSTLMTSLNCLDFEYFELCKS 304
 Db 238 VPHHVLQVLPMTLAEI-GFODTDFHOAINDAHOVTLCLLSTNCVLDPIITCFLTK 291
 QY 305 FRNSL 309
 Db 292 FRKHL 296

RESULT 13

Q9XSD4 PRELIMINARY; PRT; 342 AA.
 AC Q9XSD4
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE Platelet-activating factor receptor.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=9623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Diehl J.R., Murphy K.E., Roudgebush W.E.;
 RT "Porcine (Sus scrofa) platelet-activating factor receptor DNA."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF124054; AAD28739.2; -


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Db 146 TCVLIMAFATLSLPTALSRDVTINHP--NTVCGTLDK-----HELSHVLAIGLM 196
QY 197 ----IFMINPLIVICYTLITKELYS---YVRTGCVKVPKKVKNKVFIIIAVEPIC 248
Db 197 KSVLGFLIPFVIITVCYCLIGRALLEARVQSSRSG-----DEVLMALAAVLAFFLC 250
QY 249 FVP---FHEARIPYTLSDTRDVFDCIAENTLFYKESTIMLTSLNACIDPFIYFFLCKSF 305
Db 251 WVPHQIFHFHNV---LALLKVIENCPTLIDITDIALPFTICIAVFNSCMNPILYGFVGRNF 307
QY 306 RNSLISMKC-PNSA 319
Db 308 RNLRLRLRCGPGSA 322

```

Search completed: December 6, 2002, 10:07:59
 Job time : 104 secs

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OM protein - protein search, using sw model

Run on: December 6, 2002, 10:04:11 ; Search time 20 Seconds

(without alignments)
1643.899 Million cell updates/sec

Title: us-09-835-922-2

Perfect score: 1778

Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SQDNKKKEDGGDPNERTPM 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	394	22.2	342	2 A40191	platelet-activatin
2	392.5	22.1	342	2 S13638	platelet-activatin
3	379.5	21.3	361	2 B45680	G protein-coupled
4	366	20.6	341	2 S63666	platelet-activatin
5	362	20.4	341	2 S43252	platelet-activatin
6	357.5	20.1	308	2 I50241	G protein-coupled
7	339	19.1	359	2 S15403	angiotensin II rec
8	338	19.0	344	2 T09508	intron 17 purinerg
9	329	18.5	359	2 I39418	angiotensin II rec
10	326	18.3	359	2 S44425	angiotensin II rec
11	325.5	18.3	359	2 I48705	angiotensin II rec
12	325	18.3	359	2 A48857	protease activat
13	321	18.1	359	2 JC1104	angiotensin II rec
14	321	18.1	370	2 JC5549	heptahelical P2Y5-
15	319	17.9	359	2 A42656	angiotensin II rec
16	319	17.9	359	2 JC2134	angiotensin II rec
17	318	17.9	359	2 JC1194	angiotensin II rec
18	318	17.9	359	2 JH0621	angiotensin II rec
19	317.5	17.9	365	2 S68208	G protein-coupled
20	317.5	17.9	398	2 I56517	mu opioid receptor
21	314.5	17.7	398	2 I56504	mu opioid receptor
22	314	17.7	359	2 J01516	angiotensin II rec
23	313.5	17.6	380	2 I38435	angiotensin II rec
24	310.5	17.5	362	2 JN0694	angiotensin II rec
25	309	17.4	392	2 S65693	opioid receptor mu
26	309	17.4	400	2 I56553	mu opiate receptor
27	306	17.2	397	2 S66518	protease-activat
28	304.5	17.1	398	2 A57510	mu opioid receptor
29	299	16.8	380	2 JC2434	kappa opioid recep

30	298.5	16.8	365	2 S68679	G protein-coupled
31	298	16.8	380	2 A48227	kappa opioid recep
32	297.5	16.7	359	2 I51372	angiotensin II rec
33	297.5	16.7	360	2 A53611	interleukin-8 rece
34	297	16.7	380	2 A55259	kappa opioid recep
35	296.5	16.7	420	2 I51667	thrombin receptor
36	296	16.6	380	2 S36143	kappa opioid recep
37	295	16.6	380	2 JC2358	kappa opioid recep
38	292.5	16.5	362	2 S33733	G protein-coupled
39	291.5	16.4	373	2 A47556	ATP receptor P2u -
40	290.5	16.3	352	2 A45747	G protein-coupled
41	284.5	16.0	333	2 I38974	protein-coupled
42	282.5	15.9	352	2 G00048	fusin (LESTRA) - c
43	282	15.9	352	2 A43113	chemokine (C-C) re
44	282	15.9	355	2 J01231	interleukin-8 rece
45	281.5	15.8	353	2 S28787	neuropeptide Y/pep

ALIGNMENTS

RESULT 1
A40191
platelet-activating factor receptor - human
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 20-Jun-2000
C:Accession: A40191; JH0479; A41079; JC1359; A42831; I51923
R:Kunz, D.; Gerard, N.P.; Gerard, C.
J. Biol. Chem. 267, 9101-9106, 1992
A:Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, cell
A:Reference number: A40191; MUID:92250505; PMID:1374385
A:Accession: A40191
A:Molecule type: mRNA
A:Residues: 1-342 <KUN>
A:Cross-references: GB:M76674; NID:g456293; PIDN:AAA60002.1; PID:g456294
R:Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochran, C.G.
Biochem. Biophys. Res. Commun. 180, 105-111, 1991
A:Title: Characterization of a human cDNA that encodes a functional receptor for plat
A:Reference number: JH0479; MUID:92028922; PMID:1656963
A:Accession: JH0479
A:Molecule type: mRNA
A:Residues: 1-342 <YER>
A:Cross-references: GB:M80436; NID:g189537; PIDN:AAA60001.1; PID:g189538
A:Experimental source: granulocyte, cell line HL-60 all
R:Nakamura, M.; Honda, Z.; Izumi, T.; Sakanaka, C.; Mutoh, H.; Minami, M.; Bito, H.;
J. Biol. Chem. 266, 20400-20405, 1991
A:Title: Molecular cloning and expression of platelet-activating factor receptor from
A:Reference number: A41079; MUID:92041873; PMID:1657923
A:Accession: A41079
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-342 <NAK>
A:Cross-references: GB:D10202; GB:D90433; NID:g219975; PIDN:BA01050.1; PID:g219976
R:Sugimoto, T.; Tsuchimoto, H.; McGregor, C.G.; Mutch, H.; Shimizu, T.; Kurauchi, Y
Biochem. Biophys. Res. Commun. 189, 617-624, 1992
A:Title: Molecular cloning and characterization of the platelet-activating factor rec
A:Reference number: JC1359; MUID:93112021; PMID:1281995
A:Accession: JC1359
A:Molecule type: mRNA
A:Residues: 1-315, 'N', 317-342 <SUG>
A:Experimental source: heart
A:Note: the authors translated the codon AAT for residue 316 as Lys
R:Seyfried, C.E.; Schwelckart, V.L.; Godiska, R.; Gray, P.W.
Genomics 13, 832-834, 1992
A:Title: The human platelet-activating factor receptor gene (PTAFR) contains no intro
A:Reference number: A42831; MUID:92347886; PMID:1322356
A:Accession: A42831
A:Molecule type: DNA
A:Residues: 1-226, 'TG', 229-342 <SEY>
A:Cross-references: GB:M8177; NID:g190697; PIDN:AAA60214.1; PID:g190698
R:Chase, P.B.; Halonen, M.; Regan, J.W.;
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993

A:Title: Cloning of a human platelet-activating factor receptor gene: evidence for an 1
A:Reference number: 151923; MUID:93192035; PMID:8383507
A:Accession: 151923
A:Status: preliminary; translated from GR/EMBL/DBD
A:Molecule type: DNA
A:Residues: 15342 <RES>
A:Cross-references: GB:S56396; NID:g298580; PIDN:AAB25755.1; PID:g298581
C:Genetics:
A:Gene: GDB:PTAFR
A:Cross-references: GDB:128806; OMIM:173393
A:Map position: 1p35-1p34.3
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; transmembrane protein
E:17-38/Domain: transmembrane #status predicted <TRI>
E:54-75/Domain: transmembrane #status predicted <TRI>
E:92-113/Domain: transmembrane #status predicted <TRI>
E:134-155/Domain: transmembrane #status predicted <TRI>
E:164-205/Domain: transmembrane #status predicted <TRI>
E:223-253/Domain: transmembrane #status predicted <TRI>
E:277-297/Domain: transmembrane #status predicted <VII>

Query Match:	22.2%	Score 394;	DB 2;	Length 342;
Best Local Similarity:	32.6%	Pred. No. 1.5e-26;		
Matches 107;	Conservative 61;	Mismatches 134;	Indels 26;	Gaps 10;

[illegible]

RESULT 2
S13638
platelet-activating factor receptor - guinea pig
C:Species: *Cavia porcellus* (guinea pig)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 08-Oct-1999
C:Accession: S13638
R:Honda, Z.; Nakanura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.; Tani
Nature 349, 342-346, 1991
A:Title: Cloning by functional expression of platelet-activating factor receptor from guinea
A:Reference number: S13638; MUID:91101726; PMID:1846231
A:Accession: S13638
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-342 <HON>
A:Cross-references: CB:X56736; NID:g49442; PIDN:CAA0060.1; PID:g49443
A:Note: The species of guinea pig is not identified; In GenBank entry CCAPREC, release
A:Superfamily: ATP receptor P2u

Query Match	22.1%	Score 392.5;	DB 2;	Length 342;
Best Local Similarity	30.7%;	Pred. No. 2,1e-26;		
Matches 103;	Conservative 66;	Mismatches 146;	Indels 21;	Gaps 9;

[illegible]

Db 302 KHLSEKLNMRSSQKCSRVTDTGTMAIPINHPTV 337

RESULT 3
B45680
G protein-coupled peptide receptor EBI 2 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: B45680
R.Birkenbach, M.; Josefsen, K.; Yalamanchilli, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled
A:Reference number: A45680; MUID:93188173; PMID:8383238
A:Accession: B45680
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-361 <BIR>
A:Cross-references: GB:L08177; NID:g292056; PIDN:AAA5924.1; PID:g292057
A:Experimental source: B-lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:127096, NCBIPI:127097)
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	21.3%	Score 379.5;	DB 2,	Length 361;
Best Local Similarity	26.0%	Pred. NO. 2.9e-25;		
Matches 94;	Conservative 84;	Mismatches 152;	Indels 31;	Gaps 11;

```

0Y 1 MOADVNLE-----SAPGNSLCTRDYKLTQVLEPILLYVLEFVGLITNGLMARJEFOIRSK 56
Db 3 IOMANNEFPBPATOGNDODDIAHHSSTARIMPHYSIVELITGLVGLLADVAVOIRKK 62
0Y 57 SN-FILPLKNTVISDLMILNPEPKIL-----SDAKLG7GLRFFVOVAVSEJFEPMYI 110
Db 63 INSTLLYSNLVISDILEFTTALPRIRAVYANGPOMRIGDA-----LCRIITAVEYINIFYA 117
0Y 111 SISFELGITIDROYKTRRPFKTSNPKNLGAKILSVIIMAFMELLSLPMNI--L7NNOPR 168
Db 118 GVNEMTCSIDREFLAVVAPRLRYNKRKIRIEHAKGVCFIMWILVEAQTPLLINPMKSQEA 177
0Y 169 DKNVKKCSFELSEGGVWHELVNICOVIFIMINLYIVCYTLITKRLYS-----YVRT 223
Db 178 RITCEMYNPEEETKSLPW--ILLGACFGLYVPLIILICYSQCCLEFTRAKONPLTEK 235
0Y 224 RGCVGKPRKRVNKKVEIIIAVEFICFVDFEHARIPYLSQR--DVEDCAENLTVYKE 281
Db 226 SGVNR--KALNT--IILIVVFCFPIYHAILOHMIIKIRBSNELECCORHSFOJSLH 291
0Y 282 STLWLTSLNACLDPIYEFELCKSFERNSLIMKCPNSATSLSDONRKKEDGDGDPNEETP 341
Db 292 FTVCGLMNFNCMDPIYEFACGKIRKMYRLK--ROYSVSISSAVKAAPDENSREMETQ 350
0Y 342 M 342

```

Db 351 M 351

RESULT 4

S63666 Platelet activating factor receptor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C:Accession: S63666

R:Shi1, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.

Biochem. J. 314, 671-678, 1996

A:Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localization

A:Accession: S63666

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 <ISH>

A:Cross-references: EMBL:D50872; NID:g1256924; PIDN:BA09468.1; PID:g1256925

C:Superfamily: ATP receptor P2u

Query Match 20.6%; Score 366; DB 2; Length 341;

Best Local Similarity 29.9%; Pred. No. 4e-24;

Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;

OY 20 DYKTIQVLEPLLYTVLFVGLITNGLANRIFQI--RSKSNFI-TEKNTVISDLMLIT 76

10 DSEFRYTLPIYISVIFLGVANGYVLPVNPANLPSKLNKIKIFVNLTMADLLFLIT 69

OY 77 FPFKILSDAKLGTPRTFCQVTSVIFETMYISISFLGLITDRYQKTRPFTSNPK 136

70 LPLMIVYYNSGDMVLVNFELCNVAGCLEFINTYCSVAFLGYVYRQAVAPITQAOT 129

OY 137 NLGAKILSVYIMAFM-----FLSLPMMILTNROPDRKNKCKSEFLSESG--LVWHE 188

130 TRKGISLSLTIWISIVATASYFLATDSTNLVPKDGSNGITRCEHEPEPSVPLVYHV 189

OY 189 IVNTICQVIEIMNFI-VIVCYTLTKELKLYRSYVTRGCVPRKKNVYKFIITAVEFI 247

190 FIACFELVFLIFECNLIIVHTLTQPMRQ--RKAGV---KRRLMVCYVLAFLFI 243

OY 248 CFVPHFRIRIYTSQTRDVEDCAENTLFYKESTLMLTSLNACLDPIYFLCKSRN 307

244 CFVPHVAVLFWTLAEIG--YQTFHQAINDAHQITCLSTNCVLDPIYICFLTKRERK 301

OY 308 -----SLISMLKCPNSATS 321

302 HLEKFTYMSRSRKC-SRATS 321

RESULT 5

S43252 Platelet-activating factor receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999

C:Accession: S43252

R:Bitto, H.; Honda, Z.; Nakamura, M.; Shimizu, T.

Eur. J. Biochem. 221, 211-218, 1994

A:Title: Cloning, expression and tissue distribution of rat platelet-activating-factor-1

A:Accession: S43252; MUID:94222063; PMID:8168510

A:Molecule type: mRNA

A:Residues: 1-341 <BIT>

A:Cross-references: GB:U04740; NID:g470384; PIDN:AA18422.1; PID:g470385

C:Superfamily: ATP receptor P2u

Query Match 20.4%; Score 362; DB 2; Length 341;

Best Local Similarity 28.9%; Pred. No. 8.9e-24;

Matches 96; Conservative 66; Mismatches 120; Indels 50; Gaps 10;

OY 20 DYKTIQVLEPLLYTVLFVGLITNGLANRIF--FOIRSKSNFIIFLNKNTVISDLMLIT 76

10 DSEFRYTLPIYISVIFLGVANGYVLPVNPANLPSKLNKIKIFVNLTMADLLFLIT 69

OY 77 FPFKILSDAKLGTPRTFCQVTSVIFETMYISISFLGLITDRYQKTRPFTSNPK 136

70 LPLMIVYYNSGDMVLVNFELCNVAGCLEFINTYCSVAFLGYVYRQAVAPITQAOT 129

OY 137 NLGAKILSVYIMAFM-----FLSLPMMILTNROPDRKNKCK-----S 176

130 TRKGISLSLTIWISIVATASYFLATDSTNLVPKDGSNGITRCEHEPEPSVPLVYHI 189

OY 177 FLKSEGLVWHEIVYICQVIFWIFNLIVCYTLTKELKLYRSYVTRGCVPRKKNV 236

190 FITSCFELVFF-----LIFCYMAYII---HLLITP-----VQQRKEVRRRLAM 233

OY 237 KVFIIIAVEFICFVPHFRIRIYTSQTRDVEDCAENTLFYKESTLMLTSLNACLDPI 296

234 -VCVLAIVAFICFVPHFRIRIYTSQTRDVEDCAENTLFYKESTLMLTSLNACLDPI 290

OY 297 IYFELCKSRN-----SLISMLKCPNSATS 321

291 IYCFLLTKRKRHLSEKFTYMSRSRKC-SRATS 321

RESULT 6

150241 G protein-coupled receptor 6H1 - chicken

N:Alternate names: purinoceptor 6H1

C:Species: Gallus gallus (chicken)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Jun-2000

C:Accession: 150241; J04618

R:Kaplan, M.H.; Smith, D.I.; Sundick, R.S.

J. Immunol. 151, 628-636, 1993

A:Title: Identification of a G protein coupled receptor induced in activated T cells.

A:Reference number: 150241; MUID:93329058; PMID:8393036

A:Accession: 150241

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-308 <KAP>

A:Cross-references: GB:U06109; NID:g304383; PIDN:AA06587.1; PID:g304384

R:Webb, T.E.; Kaplan, M.G.; Barnard, E.A.

Biochem. Biophys. Res. Commun. 219, 105-110, 1996

A:Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.

A:Reference number: J04618; MUID:96190677; PMID:8619790

A:Accession: J04618

A:Molecule type: mRNA

A:Residues: 1-308 <WEB>

A:Cross-references: GB:U06109; NID:g304383; PIDN:AA06587.1; PID:g304384

A:Experimental source: T-cells

C:Comment: This receptor plays a role in T-cell activation.

C:Genetics:

A:Gene: p2y5

C:Superfamily: ATP receptor P2u

C:Keywords: G protein-coupled receptor; transmembrane protein

F:15-40/Domain: transmembrane #status predicted <TM1>

F:51-74/Domain: transmembrane #status predicted <TM2>

F:89-109/Domain: transmembrane #status predicted <TM3>

F:133-153/Domain: transmembrane #status predicted <TM4>

F:177-201/Domain: transmembrane #status predicted <TM5>

F:227-248/Domain: transmembrane #status predicted <TM6>

F:265-292/Domain: transmembrane #status predicted <TM7>

Query Match 20.1%; Score 357.5; DB 2; Length 308;

Best Local Similarity 29.5%; Pred. No. 1.9e-23;

Matches 87; Conservative 68; Mismatches 125; Indels 15; Gaps 8;

OY 14 TSLCTRDYKTIQVLEPLLYTVLFVGLITNGLANRIF--FOIRSKSNFIIFLNKNTVISDL 72

DB 3 SSMCTEDSFYKTYLGVCSWVFLGLANCAVATIFFTLKVRNRTTYMLNLAISDL 62

OY 73 MLTPFPKILSDAKLGTPRTFCQVTSVIFETMYISISFLGLITDRYQKTRPFTSNPK 132

DB 63 FVFTLFPRIIYV--VRNMPFGVDVLCISVTLFTYTMGSGISLFTGISVDRFLAIYHPPRS 121

OY 133 SNPKNLAKILSVYIMAFMFLISLPNMIL--TNROPDRKNKCK--SFLASEFGLVWHE 188

[illegible][illegible]


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Db      253  WIPHQIFEFLEVLVLIQGGIIRRCRIADIYDTAMPITIMLAYFNANCLNPLPYGGLKAKKKD 312
               ||| : | |          : | : | : | | | | | | | : |
Oy      309  LISMLK-CPNSATSIISQDNRK 328
               :: | |   | | | | : |
Db      313  ILQLKLKYIPRAKASHSNLSTK 333

RESULT 10
S44425
angiotensin II receptor type 1 - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S44425
R:Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.
FEBS Lett. 343, 146-150, 1994
A:Title: Molecular cloning of the canine angiotensin II receptor. An AT1-like receptor
A:Reference number: S44425; MUID:94222188; PMID:8168620
A:Accession: S44425
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-359 <MBUR>
A:Cross-references: PIDD:AAB30674.1; PID:g546569
A:Experimental source: liver
A:Superfamily: vertebrate rhodopsin

```

Query Match	18.3%	Score 326	DB 2	Length 359
Best Local Similarly	29.28%	Pred. No. 1.2e-20		
Matches 92	Conservative 54	Mismatches 147	Indels 22	Gaps 8

OY 26 VLEPILTYVLEFVGGLITNGL-AMRIEPIRKSKNFIIFLKNTVISDLMILTPEFKIISD 84
| : | : : | : | : | : | : | : | : | : | :
DB 29 VMIPPLYSIIFFVGVIGNSLVIVIVIFYFMKKTKTASVSFLNLALDDCFELLPIMAVYT 88

QY 85 AKLGGPLRFVCCQYSVFETMTYSISFGLITIDRYCKTTRPKTSNPKNLGAKIL 144
| :::: | : | : | : | :
Db 89 AMEYRMPEFGNYLCKIASASVSFNLYASFLLTCISIDRYAIVHPKSPVRRTMLMAKV 148

QY 145 SVVIAFMFLSLPNMILT-NQPRDKVKKCSF-----LKSEGLVMEIVANICQ 199
::|| | || : | : : | : :
Db 149 CIIWLAGLASLPITIIHRVFEIENTNITVCARHYEQNSTLPGLGLT-KNIIIGFL-- 209

```

QY 196 VIFMNFLLIIVCYTTLTKELXRSYVFRGCVKPRKRVNVKVF-IIAVFICFVPEHF 256
      ||:: |||| | |:: | | |:: | |:: | |
Db 206 ---FPFLILTSYTLIWKTLKRAYEIOK--NKPRNDIFKIIMAVLFFFSWVPQI 256

```

QY 255 ARIPTLSQRDVFDCDAENTLEFYKESTLWLFSLNACDPIFYFLFLCKSFNSLSIMLK 314

Db 259 FTFLDLVLIGLGIHDCKIADIVDTAMPITICIAFYENNCNLPLFYGLGKKPKFYFLQLK 318

QY	315	-CPNSATSLSQDNRK	328
		:	
Db	319	YIPPAKSHSLSTK	333

RESULT 11
I48705
proteinase activated receptor 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision: 02-Jul-1996 #text_change: 24-Nov-1999
C:Accession: I48705
J:Mytseth, S.; Larsson, A.K.; Aberly, H.; Sundellin, J.
J. Biol. Chem. 270, 5950-5955, 1995
A:Title: The mouse proteinase-activated receptor-2 cDNA and gene. Molecular cloning and
A:Reference number: I48705; MUID:95197620; PMID:7890726
A:Accession: I48705
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-399 <RES>
A:Cross-References: EMBL:Z48043; NID:g663020; PIDN:CA488097.1; PID:g663021
C:Superfamily: ATP receptor P2u

Query match 18.38; Score 325.5; DB 2; Length 399;

```

Best Local Similarity 27.6%, Pred. No. 1.5e-20.
Matches 92; Conservative 73; Mismatches 141; Indels 27; Gaps 12.

QY 22 KITQVLFPLLYTVLVEFGVLTNGLAMRI-FQIRSKSNEIIFLAKNTVSDLMILTFPEPK 80
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 74 KLTFFLFPLVYVYIIVVIGIRPSGMALMIFFLFTKKKHRAVIYIMADLADLSVIMFPLK 133
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 81 ILSDAKLGTPLRTEPCOVATSVIIFYFTWYISISFLGLITIDRYOKTTRPRKTSNPKNLG 140
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 134 ISYHLHGNNWVYGAELCKVYLIGFEFGNMYCSILFMTCLSQYRWYIVNDM--GHPRKAN 191
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 141 AKI-LSVYIMAFMLSLSPNML--TNROPDKNNKCSFLKSEGLVHWHELYVNTICOV- 196
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 192 IAVGSIAIMILLIFVTTIPLYVMKOTIYIPA-LNTTCHADVPEEVLV-GDMFNFLSLA 249
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 197 --IFINILFLIVVCTLTLLTKELRSYVVRKGVGKPRKKVANKVITIIIAVFETCVPRIF 254
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 250 IGVFLFPALLTPASAVVLMIKLTSSAMDEHSSEK--RQRAIRLITVLVAMYFICAPASML 307
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 255 AR-IPYTLISQFDVDCDAENTLFEVVKESTLMLTSLGNCLDPIFYFLCKSRNSLISML 313
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 308 ILVAVHYFLIKTY-----RQSHVVALIYVALCTLSLNSCIDPEFYVYFVSKDFRDHARNAL 361
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 314 KCPNSAT-----SLSDNRKKKEODGDPNEET 340
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 362 LCRSVRYTVNRMQISLS-SKFSRKKGSYSSSST 393
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 12
AA8857

C:Species: *Oryctolagus cuniculus* (domestic rabbit)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A48857

Am. J. Physiol. 264, F645-F654, 1993
A1:Title: Cloning of a rabbit kidney cortex A11 angiotensin II receptor that is present
A1:Reference number: A48857; MUID:93236091; PMID:7916579

A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-359 <BUR>

A: Experimental source: proximal tubule cells
A: Note: sequence extracted from NCBI backbone (NCBIN:129600, NCBI P:129601)
C: Superfamily: vertebrate rhodopsin

Query Match	18.3%	Score 325;	DB 2;	Length 359;
Best Local Similarity	29.2%	Pred. NO. 1.5e-20;		

26 VFPLLYTVLEFVGILNGLA-MRIFFQIRSKSNFIIFLKNVTISDLMILTEPFKILSD 84

85 AKLGTPLRFEVCQVTSVIEFFMYISISFLGLTIDRYOKTRPEKTSNPKNLGAKIL 144

```
QY      145 SVVIAFMFLSLPNMILT-NRPRDKNVKCSF-----LKSEGLVWHEIVNYICQ 195
```

OY 196 VIFWNEFLIVCYTLITKELXSYVFRGCVGVPRKKVNKVFI-IIAVFICFVPHEH 25
 ||::| | | | : :: | | : : | : | :
D8 206 - --DNDERTTMEVETLTKALPVAKVTOR-- --WDNDODCTRTIATUV RPPEDDLADYAR JEC-

QY 255 ARIPTYLSQTRDVEDCTAENTLFYVKESTLMTSLNACLDPEIFYELCKSSFRNSLISMK 314
 | | | | : : | | | | | | | : : | |
 Ds 250 EEMEDVITOTGVITUPPDAADITDIAADTETCTAENWGGTNDT EYCKGCKREVEVEVOTR 310

QY 315 - CPNSATSLSDNRK 328

